

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2004, 09:24:21 ; Search time 129 Seconds  
(without alignments)  
578.740 Million cell updates/sec

Title: US-10-088-945A-10  
Perfect score: 1195  
Sequence: 1 MAERDLRLGAWSPFALRV.....KLVEFAKILQKWAARAAK 232

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pdb.\*
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pdb.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pdb.\*
- 4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pdb.\*
- 5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pdb.\*
- 6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pdb.\*
- 7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pdb.\*
- 8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pdb.\*
- 9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUBCOMB.pdb.\*
- 10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUBCOMB.pdb.\*
- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pdb.\*
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pdb.\*
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pdb.\*
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pdb.\*
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pdb.\*
- 16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pdb.\*
- 17: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pdb.\*
- 18: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	96.7	233	12	US-10-424-599-194349
2	1000.5	83.7	234	12	US-10-424-599-200780
3	624	52.2	233	9	US-09-765-213A-4
4	623	52.1	233	9	US-09-765-213A-2
5	607	50.8	233	9	US-09-765-213A-6
6	573	47.9	233	16	US-10-437-963-153017
7	557.5	46.7	375	16	US-10-437-963-154851
8	542	45.4	305	16	US-10-437-963-131794
9	541	45.3	244	16	US-10-437-963-117929
10	540	45.2	235	16	US-10-437-963-148018
11	535.5	44.8	237	16	US-10-437-963-152885
12	535	44.8	243	16	US-10-437-963-148024
13	534	44.7	236	16	US-10-437-963-132134
14	533	44.6	336	16	US-10-437-963-130681
15	528	44.2	232	16	US-10-767-701-45399

16	525.5	44.0	233	16	US-10-437-963-109052	Sequence 109052,
17	523.5	43.8	233	16	US-10-776-956-16	Sequence 16, Appl
18	522.5	43.7	237	16	US-10-437-963-204635	Sequence 204635,
19	521	43.6	241	16	US-10-437-963-152637	Sequence 152637,
20	519.5	43.5	233	16	US-10-437-963-186789	Sequence 186789,
21	514.5	43.1	236	9	US-09-765-213A-9	Sequence 9, Appl
22	514	43.0	240	16	US-10-437-963-144283	Sequence 144283,
23	512	42.8	264	16	US-10-437-963-109053	Sequence 109053,
24	511.5	42.8	233	16	US-10-437-963-186791	Sequence 186791,
25	511	42.8	269	12	US-10-425-114-50727	Sequence 8, Appl
26	511	42.8	269	12	US-10-425-114-66732	Sequence 66732, A
27	508.5	42.6	229	9	US-09-765-213A-8	Sequence 8, Appl
28	506.5	42.4	354	16	US-10-437-963-151237	Sequence 151237,
29	504	42.2	235	16	US-10-437-963-106610	Sequence 106610,
30	501.5	42.0	241	16	US-10-767-701-45167	Sequence 45167, A
31	501.5	42.0	248	12	US-10-425-114-52797	Sequence 52797, A
32	501	41.9	237	12	US-10-425-114-62288	Sequence 62288, A
33	498.5	41.7	226	16	US-10-767-701-39274	Sequence 39274, A
34	498	41.7	256	12	US-10-425-114-52786	Sequence 52786, A
35	497	41.6	230	16	US-10-437-963-170660	Sequence 170660,
36	493	41.3	240	16	US-10-437-963-202064	Sequence 202064,
37	489	40.9	225	9	US-09-765-213A-7	Sequence 7, Appl
38	486.5	40.7	243	16	US-10-437-963-154488	Sequence 154488,
39	486	40.7	232	16	US-10-767-701-43039	Sequence 43039, A
40	484.5	40.5	245	12	US-10-425-114-72039	Sequence 72039, A
41	483	40.4	245	12	US-10-425-114-53472	Sequence 53472, A
42	483	40.4	245	12	US-10-425-114-72237	Sequence 72237, A
43	480	40.2	234	16	US-10-437-963-161253	Sequence 161253,
44	469	39.2	263	12	US-10-425-114-62056	Sequence 62056, A
45	456	38.2	257	16	US-10-437-963-148917	Sequence 148917,

ALIGNMENTS

RESULT 1

US-10-424-599-194349  
; Sequence 194349, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 194349  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(233)  
; OTHER INFORMATION: unsure at all Xaa locations  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_17524C.1.pep  
; OTHER INFORMATION: PAT\_MRT3847\_17524C.1.pep  
US-10-424-599-194349

Query Match	96.7%	Score	1155.5	DB	12	Length	233	Indels	1	Gaps	1
Best Local Similarity	97.0%	Pred. No.	7.7e-108								
Matches	226	Conservative	2	Mismatches	4						
Qy	1	MAERDLRLGAWSPFALRVQIALNKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH	60								
Db	1	MAERDLRLGAWSPFALRVQIALNKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH	60								
Qy	61	GDKVCBSAIIIVEYDVEWNNALSIPLQAYDRANARFWYSYIDDKWLSKSV-LATE	119								
Db	61	GDKVCBSAIIIVEYDVEWNNALSIPLQAYDRANARFWYSYIDDKWLSKSV-LATE	120								

CIP at 09/985,678  
which is COW at 09/  
304,317 (5/6/99)  
- both parts are CRPE  
but do not show a hit  
in pending database  
so appears seq. is  
the CIP

RESULT 3  
 US-09-765-213A-4  
 ; Sequence 4, Application US/09765213A  
 ; Patent No. US20020079846A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Facchini, Peter J  
 ; TITLE OF INVENTION: No. US20020079846A1el Glutathione-S-Transferase Nucleic Acids and  
 ; TITLE OF INVENTION: Polypeptides and Methods of Use  
 ; FILE REFERENCE: 22542-001  
 ; CURRENT APPLICATION NUMBER: US/09/765,213A  
 ; CURRENT FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION NUMBER: 60/176708  
 ; PRIOR FILING DATE: 2000-01-18  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 233  
 ; TYPE: PRT  
 ; ORGANISM: *Papaver somniferum*

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RES001_5
US-09-765-213A-6
; Sequence 6, Application US/09765213A
; Patent No. US20020079846A1
; GENERAL INFORMATION:
; APPLICANT: Facchini, Peter J
; TITLE OF INVENTION: Polypeptides and Methods of Use
; TITLE OF INVENTION: Polypeptides and Methods of Use

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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 117929
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2128C.1.pep
US-10-437-963-117929

Query Match 45.3%; Score 541; DB 16; Length 244;
Best Local Similarity 49.3%; Pred. No. 5.9e-46;
Matches 108; Conservative 41; Mismatches 58; Indels 12; Gaps 3;

QY 6 LRLIGAFSPPALRVQIALNKLGLDYEYVVEETLNPKSELLKSNPVHKKIPVFFHGDKVI 65
DB 15 VRLVGGWASPFTNRVVVALKLVGVEHEMLQBTGVKSELLRSNPVHKKIPVLLHHSKPL 74
QY 66 CESALIVEYIDVW---SNNALSILPONAYDRANARFWYSYIDDKWLTSLK----SVLAT 118
DB 75 PSLVIVEYIDEVWSPASNGGAPAILPRDPHGAVRFFWARYVDDKILPLGLRVLRGSVAGD 134
QY 119 EDEAKKLHFEQAEVLEKVEVFNKCSGKAYFGGDTIGFVDIGFGSFLSFIRVSENMN 178
DB 135 KDOTAGEM-----STTLQRLBEAFVKCSQKKEYFGGDSIGYLDIALGSLGFWIKAVEKIA 189
QY 179 EKKLDETKYPGCLTIWAETFAADPAVKGLLPETEKLVF 217
DB 190 GVELLNETKPLTIAYMADRFCAPHAIVDVDPADKLVEF 228

RESULT 10
US-10-437-963-148018
; Sequence 148018, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 148018
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48491C.1.pep
US-10-437-963-148018

Query Match 45.2%; Score 540; DB 16; Length 235;
Best Local Similarity 46.8%; Pred. No. 7.1e-46;
Matches 108; Conservative 44; Mismatches 71; Indels 8; Gaps 3;

QY 5 DURLIGAFSPPALRVQIALNKLGLDYEYVVEETLNPKSELLKSNPVHKKIPVFFHGDKV 64
DB 7 ELKLLGMWTSPPALRVKIALSFKGLSYEYABEDLSNKSSELLSNPNVHKKIPVLLIHNGKP 66
QY 65 ICESALIVEYIDVWNNALSILPONAYDRANARFWYSYIDDK----WLTSKSVLATE 120
DB 67 ICESQVIVQYIDAEAPFGAGVPLPSDPPERAVARFWAAYIDDKLLKSWLQA--SMGKTEE 124

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Db 123 SKTEERAAVAQAVALLETLEGAFGCSKGFPGGCVGVVDVVLGGYLGWFTADKL 182  
Qy 178 NERKLLDETKYPGLTWAETFAADPAVKGLLP-ETEKLVFAKILQLKWAASAA 230  
Db 183 IGRLLIDPARTPALAAWEERFRATDAAGVVPDDADKLLERQTL-LRWSASKA 235

RESULT 14

US-10-437-963-130681  
; Sequence 130681, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 130681  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(336)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_3281C.1.pap  
US-10-437-963-130681

Query Match 44.6%; Score 533; DB 16; Length 336;  
Best Local Similarity 48.3%; Pred. No. 5.9e-45;  
Matches 115; Conservative 37; Mismatches 70; Indels 16; Gaps 4;  
Qy 6 LRLIGAWPSPFALRVQIALNLKGLDYEVVETLNPKSELLKSNPVHKKIPVFFHGDKVI 65  
Db 98 VRVVGWASPFMNRVVALKLGVEHEMLQETVGKSELLRSNPVHKKIPVLLHHGKPI 157  
Qy 66 CESALIIVEYDEVW--SNNALSILPONAYDRANARFVSYIDDK-----WLTSLSKSLA 117  
Db 158 AESLIIVYIDEVWPASDGAPAILPRDPYCAVERFWAQYIDDKPDDFALLIDNLCAVSS 217  
Qy 118 ----TEDDEAKLHFEQAEEVLEKVEEVFNKCSGKAYFGGDTIGFVDIGFGSFLSFRV 173  
Db 218 GDSVERNRGRGTIVENSTALKHLEAFVKCSQGGKYGDKIGYLDIALGSLGWIKA 277  
Qy 174 SENNERKLLDETKYPGLTWAETFAADPAVKGLLPETEKLVFAKILQLKWAASAAA 231  
Db 278 VEKPAVELLDEAKVPLNLAADRFCAHPAVVDAMPADKLVFEFA----VKHAAASMK 331

RESULT 15

US-10-767-701-45399  
; Sequence 45399, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 45399  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10423\_1.pap  
US-10-767-701-45399

Query Match 44.2%; Score 528; DB 16; Length 232;  
Best Local Similarity 47.7%; Pred. No. 1.1e-44;  
Matches 106; Conservative 40; Mismatches 68; Indels 8; Gaps 3;  
Qy 1 MAERDLRLIGAWPSPFALRVQIALNLKGLDYEVVETLNPKSELLKSNPVHKKIPVFFH 60  
Db 1 MSEADVVRVIGLWSPFPFVIRVLIALKLGVEYELVEEVGKSELLRSNPVHKKIPVLLH 60  
Qy 61 GDKVICESALIIVEYDEVWSSNNALS-ILPONAYDRANARFVSYIDDKMLTSLKSLATE 119  
Db 61 HGKPISESLIIVQYIDEVWSSDTPAFLLPADPYTRAVHRFWAQYVDDKLPPIRLRGTD 120  
Qy 120 ---DDEAKLHFEQAEEVLEKVEEVFNKCSGKAYFGGDTIGFVDIGFGSFLSFRVSEN 176  
Db 121 GGGKDEAA---EQLSAAQLLEEAFTKLSQGHYFGSDSGVYLDIALVSVGVGWKAVEK 176  
Qy 177 MNERKLLDETKYPGLTWAETFAADPAVKGLLPETEKLVFEFA 218  
Db 177 MAGVTLLDKAKVPLNLAADRLCNHFAVVESIPDADKFEVFS 218

Search completed: October 8, 2004, 09:36:12  
Job time : 132 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	1000.5	83.7	234	10	Q9F0F3	Q9f0f3 glycine max	
2	638	53.4	227	10	Q9FUS9	Q9fus9 arabidopsais	
3	632	52.9	227	10	Q9FUS8	Q9fus8 arabidopsais	
4	624	52.2	233	10	Q9SEK1	Q9sek1 papaver som	
5	623	52.1	233	10	Q9S7N6	Q9s7n6 papaver som	
6	622	52.1	227	10	Q94110	Q94110 arabidopsais	
7	617.5	51.7	281	10	Q9M6R4	Q9m6r4 gossypium h	
8	596	49.9	234	10	Q9X1F8	Q9x1f8 arabidopsais	
9	595	49.8	207	10	Q9FUS7	Q9fus7 arabidopsais	
10	587	49.1	234	10	Q94K12	Q94k12 arabidopsais	
11	573	47.9	233	10	Q9FUE3	Q9fue3 oryza sativ	
12	563.5	47.2	226	10	Q9FV19	Q9fv19 petroselinu	
13	558	46.7	233	10	Q9LQ48	Q9lq48 arabidopsais	
14	557.5	46.7	231	10	Q945W4	Q945w4 oryza sativ	
15	554	46.4	233	10	Q8LF83	Q8lf83 arabidopsais	
16	541	45.3	235	10	Q8S715	Q8s715 oryza sativ	

QY 63 ICESAT1VEITIDEVMSNNALSTIEFQNAIDGAGARTWVSGIIDE



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DR InterPro: IPR004045; GST_Nterm.
DR Pfam: PF00043; GST_C; 1.
DR Pfam: PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 233 AA; 26017 MW; C5A1376BC0D83B40 CRC64;

Query Match 52.2%; Score 624; DB 10; Length 233;
Best Local Similarity 54.0%; Pred. No. 2.4e-44;
Matches 116; Conservative 39; Mismatches 60; Indels 0; Gaps 0;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8 EVKILGWPSPFVVRPRLIALNKSVKYLLEETFGSKSELLKSNPIYKPIVPMIHGDKP 67

Qy 65 ICESAIIIVEYIDVWSNNALSILPQAYDRANARFWVSYYDDKWLTSKSVLATEDEAK 124
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68 ICESMIIVQYIDVWASAGHSIIIPSDYDASIAFWATYIDDKFPFSLMGIASKDAEEK 127

Qy 125 KLHFEQAEVLEKVEEVFNKCEKAYFGGDTIGFDIGFSGFSLFIRVSNMNERKLLD 184
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
128 KAAIEQAIAFGIIEEAYQKTSKGDFFGGEKIGYIDIAFGCYIGWIRVTEKMGKILFD 187

Qy 185 ETKYPGTLTWAETFAADPAVKGLLPETEKLVFAK 219
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
188 ETKVPGTLTKWAETFAADPAVKGLLPETDLMFAK 222

RESULT 5
Q9S7M6 PRELIMINARY; PRT; 233 AA.
AC Q9S7M6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase 2 (EC 2.5.1.18).
OS Papaver somniferum (Opium poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Papaver.
OX NCBI_TaxID=3469;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. MARIANE;
RA Pacchini P.J., Yu M.;
RT "Molecular cloning and characterization of a glutathione S-transferase
RT gene family from opium poppy."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118925; AAP22517.1; -
DR EMBL; AF118924; AAP22517.1; -
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 233 AA; 25945 MW; 72FF3137BC295CDD CRC64;

Query Match 52.1%; Score 623; DB 10; Length 233;
Best Local Similarity 54.0%; Pred. No. 2.9e-44;
Matches 116; Conservative 39; Mismatches 60; Indels 0; Gaps 0;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8 EVKILGWPSPFVVRPRLIALNKSVKYLLEETFGSKSELLKSNPIYKPIVPMIHGDKP 67

Qy 65 ICESAIIIVEYIDVWSNNALSILPQAYDRANARFWVSYYDDKWLTSKSVLATEDEAK 124
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68 ICESMIIVQYIDVWASAGHSIIIPSDYDASIAFWATYIDDKFPFSLMGIASKDAEEK 127

Qy 125 KLHFEQAEVLEKVEEVFNKCEKAYFGGDTIGFDIGFSGFSLFIRVSNMNERKLLD 184
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
128 KAAIEQAIAFGIIEEAYQKTSKGDFFGGEKIGYIDIAFGCYIGWIRVTEKMGKILFD 187

Qy 185 ETKYPGTLTWAETFAADPAVKGLLPETEKLVFAK 219
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
188 ETKVPGTLTKWAETFAADPAVKGLLPETDLMFAK 222

RESULT 6
Q94II0 PRELIMINARY; PRT; 227 AA.
AC Q94II0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase.
GN ERD9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Shinozaki K., Yamaguchi-shinozaki K., Takahashi S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=94355652; PubMed=8075396;
RA Kiyosue T., Yamaguchi-shinozaki K., Shinozaki K.;
RT "Cloning of cDNAs for genes that are early-responsive to dehydration
RT stress (ERDs) in Arabidopsis thaliana L.: identification of three ERDs
RT as HSP cognate genes.";
RL Plant Mol. Biol. 25:791-798(1994).
DR EMBL; AB039930; BAB63917.1; -
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 227 AA; 25246 MW; 70A6FD56B98C9BB2 CRC64;

Query Match 52.1%; Score 622; DB 10; Length 227;
Best Local Similarity 54.8%; Pred. No. 3.4e-44;
Matches 120; Conservative 32; Mismatches 67; Indels 0; Gaps 0;

Qy 1 MAERDLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MASSDVKLIGAWASPFVVRPRLIALNLKSVPEYFLOETFGSKSELLKSNPVHKKIPVLLH 60

Qy 61 GDKVICSAIIIVEYIDVWSNNALSILPQAYDRANARFWVSYYDDKWLTSKSVLATEDEAK 120
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ADKPVSESNIIIVEYIDVWSSGSPSILPSPDYDRAMARFWAAYIDKMFVALRGFLKAGG 120

Qy 121 DEAKLHFEQAEVLEKVEEVFNKCEKAYFGGDTIGFDIGFSGFSLFIRVSNMNER 180
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 EEEKKAVIAQLEGNFALEKAFIDCSKGKSFNGDNIYGLNIALGCLFALVRVTELAHSVY 180

Qy 181 KLIDETKPYGLTWAETFAADPAVKGLLPETEKLVFAK 219
Dy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 KLIDETKPSLKWAEFNCNDPAVKPVPETAKLAEFAK 219

RESULT 7
Q9M6R4 PRELIMINARY; PRT; 281 AA.
AC Q9M6R4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase.
OS Gossypium hirsutum (Upland cotton).
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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Fiber;
RA Kang W.H., Yamamoto E., Allen D.R.;
RT "Cloning and characterization of glutathione S-transferase (GST) gene
from cotton plants (Gossypium hirsutum L. cv. Coker 312).";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159229; AAF29773.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferase.
SQ SEQUENCE 281 AA; 31803 MW; 75B09DD3C866BFDC CRC64;
Query Match 51.7%; Score 617.5; DB 10; Length 281;
Best Local Similarity 53.2%; Pred. No. 1.1e-43;
Matches 118; Conservative 42; Mismatches 59; Indels 3; Gaps 2;
Qy 2 AERDLRLIGAWFSPFALRVQIALNLKGLDYVEVEETL-NPKSELLKSNPVHKKIPVFFH 60
Db :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
53 SDAEVKVLGTWASPFVMRVRIALNIKSVAYBFLQERLWEGKSELLKSNPVHKKIPVLIH 112
Qy 61 GDKVICESAIIVEYIDVWNNALSILPQAYDRANARFWSYIDDKWLTSLSKSVLATE 120
Db || || || || || || || || || || || || || || || || || || || || || ||
113 GDDTICSELIIVQYIDEVWP--SVPILPSPDPERAAARFAAAYLDDDKWFFSLRAIGMAEG 170
Qy 121 DEAKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTIGFVDVIGFGSFLSFRVSENMMER 180
Db :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
171 EDARKAAGVVEGEMLEEFAGFCQSQOALFGKQIGYLDITGCGFLGHLRVTEKMSGI 230
Qy 181 KLLDETKYPGLTLWAEATFAADPAVKGLLPETEKLVFAKILQ 222
Db || || || || || || || || || || || || || || || || || || || || || ||
231 KLLNEINTPALLKWNARFENDAAVKDVMPETEKLAFAKMLR 272
RESULT 8
Q9XIF8 PRELIMINARY; PRT; 234 AA.
AC Q9XIF8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F23H11.1 protein (T30E16.30).
GN F23H11.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Federpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J.R., Theologis A., Davis R.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S.,
RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
RA Federpiel N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome
I.";
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RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federpiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007258; AAD39312.1; -.
DR EMBL; AC009317; AAF79760.1; -.
DR PIR; F96620; F96620.
DR InterPro; IPR004045; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
SQ SEQUENCE 234 AA; 26506 MW; F744F7C93A81E843 CRC64;
Query Match 49.9%; Score 596; DB 10; Length 234;
Best Local Similarity 49.6%; Pred. No. 5.4e-42;
Matches 115; Conservative 46; Mismatches 69; Indels 2; Gaps 2;
Qy 1 MAER-DLRLIGAWFSPFALRVQIALNLKGLDYVEVEETL-NPKSELLKSNPVHKKIPVF 58
Db 1 MGEKEEVKLGWVSPVAIRPKIALRLKSDYDYVEENLFGSKSELLKSNPVHKKVPVL 60
Qy 59 FHGDKVICESAIIVEYIDVWNNALSILPQAYDRANARFWSYIDDKWLTSLSKSVLAT 118
Db || || || || || || || || || || || || || || || || || || || || || ||
61 LHNNKPIVESLNIYEYIDETWSSAPSLPSPHYDRALARFWSDFVNDKWFPAALRMAIT 120
Qy 119 EDDEAKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTIGFVDVIGFGSFLSFRVSNMN 178
Db :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
121 KSEDAKAKAMEVEEGLEQLDEDAFVSISKGRPFPGGAIGFMDICFGSFVLLKAREKFK 180
Qy 179 ERKLLDETKYPGLTLWAEATFAADPAVKGLLPETEKLVFAKILQKWAASAA 230
Db || || || || || || || || || || || || || || || || || || || || || ||
181 AEKLLDESKTPTSLCKWADRFSLDSTVKVNAPEIEKVAEFLQELEVRAQSAAS 232
RESULT 9
Q9FUS7 PRELIMINARY; PRT; 207 AA.
AC Q9FUS7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase.
GN GST30B.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Wagner U., Mauch F.;
RT "Analysis of the Glutathione S-transferase family in Arabidopsis
thaliana."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288192; AAG30141.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
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DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 207 AA; 23049 MW; 98149A1E4FAABE8 CRC64;

Query Match 49.8%; Score 595; DB 10; Length 207;
Best Local Similarity 52.5%; Pred. No. 5.6e-42;
Matches 115; Conservative 29; Mismatches 55; Indels 20; Gaps 1;

Qy 1 MAERDLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MASSDVKLIGAWSPFVMPRIALNLKSPVEPQETFGSKSELLKSNPVHKKIPVLLH 60

Qy 61 GDKVICSAIIVEIDVWNSNALSILPQAYDRANARFWVSYYDDKWLTSLSKVLATD 120
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ADKPVSESNIIVEYIDTWSGSGSILPSPYDRAMARFWAAYIDKFWALRGFL---- 116

Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAVFGDITGFDVIGFGSFLSFIRVSENMMN 180
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 -----KAGGAFIDCSGKGFNFNGDNLGYLDIALGCFGLAWLRVTELAHSV 160

Qy 181 KLDDETKYPGLTWAETFAADPAVKGLLPETEKLVFAK 219
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 KILDEAKTPSLSKWAENFCNDPAVKPWPETAKLAEPK 199

RESULT 10
Q94K12 PRELIMINARY; PRT; 234 AA.
AC Q94K12;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Similar to glutathione S-transferase.
GN T30E16.30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.,
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF370480; AAK43857.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 234 AA; 26490 MW; EBA4F7D6DA81E843 CRC64;

Query Match 49.1%; Score 587; DB 10; Length 234;
Best Local Similarity 49.1%; Pred. No. 3.1e-41;
Matches 114; Conservative 46; Mismatches 70; Indels 2; Gaps 2;

Qy 1 MAER-DLRLGAWFSPFALRVQIALNLKGLDYEVVEETL-NPKSELLKSNPVHKKIPV 58
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MGEKEVKLLGVWYSPVAIRPKIALRLKSVDYDVVEENLFGSKSELLKSNPVHKKVPVL 60

Qy 59 FHGDKVTCESAIIVEYIDVWNSNALSILPQAYDRANARFWVSYYDDKWLTSLSKVLAT 118
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 LHNNKPIVESLNIIVEYIDETWSSAPSILPSHPYDRALARFWSDFVNDKMPFALRMAIT 120

Qy 119 EDDAKKLHFPQAEVLEKVEEVFNKCSGKAVFGDITGFDVIGFGSFLSFIRVSENMMN 178
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 KSDAKAKAMEEVBEGLLQLEDAFVSIKGPFFGGAIGFMDICFGSVLLKAREKFK 180
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Qy 179 ERKLDDETKYPGLTWAETFAADPAVKGLLPETEKLVFAKILQKWAASAA 230
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 AEKLVESKTPSLCKWADFLSDETVKNVAPEIEKVAEFLQLELVRAQSAAS 232

RESULT 11
Q9FUE3 PRELIMINARY; PRT; 233 AA.
AC Q9FUE3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Putative glutathione S-transferase.
GN OSJNBA0034L04.7 OR OSJNBA0038A07.10.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Soranzo N., Frova C., Rizzardi R., Sari-Gorla M.;
RA "Characterization of EST clones encoding for glutathione S-
RA transferases in Oryza sativa (L.)";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Vanaken S.S.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RA "Oryza sativa chromosome 10 BAC OSJNBA0034L04 genomic sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Frazer C.M.;
RA "Oryza sativa chromosome 10 BAC OSJNBA0038A07 genomic sequence.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RA "In-depth view of structure, activity, and evolution of rice
RA chromosome 10.";
RL Science 300:1566-1569(2003).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF309379; AAG32472.1; -.
DR EMBL; AC091680; AAM12325.1; -.
DR EMBL; AC113948; AAM94544.1; -.
DR EMBL; AE017114; AAP54745.1; -.
DR Gramene; Q9FUE3; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferrase.
SQ SEQUENCE 233 AA; 25332 MW; C80416E1EA81CBD5 CRC64;

Query Match 47.9%; Score 573; DB 10; Length 233;
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ID	Q9LQ48	PRELIMINARY;	PRT;	233 AA.
AC	Q9LQ48;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	T30E16.25			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsia.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,			
RA	Altati H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,			
RA	Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luross S.,			
RA	Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,			
RA	Federspiel N.A., Theologis A., Ecker J.R.;			
RT	"Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome			
RT	I.";			
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ecker J.R.;			
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Ecker J.R.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,			
RA	Khan S., Kim C., Altati H., Bei B., Chin C., Chiou J., Choi E.,			
RA	Conn L., Conway A., Gonzalez A., Hansen N., Hwang B., Koo T., Lam B.,			
RA	Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharasy N.,			
RA	Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,			
RA	Thavari A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,			
RA	Theologis A., Ecker J.;			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC009317; AAF79758.1; -			
DR	PIR; D96620; D96620.			
DR	InterPro; IPR004046; GST_Cterm.			
DR	InterPro; IPR004045; GST_Nterm.			
DR	Pfam; PF00043; GST_C; 1.			
DR	Pfam; PF02798; GST_N; 1.			
SQ	SEQUENCE 233 AA; 26535 MW; 8722CA2CE7AEC09D CRC64;			
Query Match 46.7%; Score 558; DB 10; Length 233;				
Best Local Similarity 48.4%; Pred. No. 8.3e-39;				
Matches 106; Conservative 42; Mismatches 69; Indels 2; Gaps 2				
QY	1 MAER-DLRLLGAWFPPALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVF 58			
DB	1 MGEREVEKLLGTWYSPVIRAKRLRLKSVDDYVEEDLFGSKSELLKSNPIFKKVPVL 60			
QY	59 FHGDKVICSATIIVEYDEWNSNALSILPQAYDRANARFWSYIDDKWLTSLKSVLAT 118			
DB	61 IHTKPCVSLNIVEYIDETWNSGSSILPSHPYDRLARFWSVFDKMLPTLMAA 120			
QY	119 EDDEAKHLFEQAEVLEKVEEVFNKCEGKAYFGDGTIGFVIGFGSFLFIRVSENN 178			
DB	121 KSEAKAKMGVEEGLQLQEAFAIALSKGSFFGGETIGFIDICLGSFLVLLKAREKL 180			
QY	179 ERKLLDETQYPGTLTWAETFAADPAVKGLPETEKLVF 217			
DB	181 NEKILDELATPSLYRWANQFLSNEMVKNVPPDIDKAKE 219			
RESULT 14				
ID	Q945W4	PRELIMINARY;	PRT;	231 AA.
AC	Q945W4;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			





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Best Local Similarity 40.7%; Pred. No. 1.5e-27;
Matches 94; Conservative 46; Mismatches 80; Indels 11; Gaps 5;

Qy 3 ERDLRLGAFSPALRVOIALNLKGLDYEVVEETLNPKESELLKSNPVHKKIPVFFHG 62
Db 5 QEDVKLLGIVGSPFCRVOIALKLGVEYKELEENLGNKSDLLKYNPVHKKVPVFFHNE 64
Qy 63 KVICESAIIVEYIDEVWSNNALSILPQAYDRANARFWVSYYDDKWLTSLSKSVLAT 122
Db 65 QPIAESLIVIEYIDETWKN--PILPSPYQALARFWSKFDIDKIVGAVSKSVFTVDEK 122
Qy 123 AKULHFEQAEVLEKVEEVFNKCSGKAYFGDITGFDIGFGSFLSF-IRVSNMNERK 181
Db 123 ERENKVEEYALQFLENEL---KDKKFFGCEBFGLVDA-AVFIAFWIPFQIEIAGLQ 177
Qy 182 LLDKTKPGLTLWAETFAADPAVKGLLPETEKLVFAKILQKWAASAAAK 232
Db 178 LFTSEKFPILYKWSQEFNLHPFVHEVUPPRDPLPAYFK---ARYESUSASK 225

RESULT 2
GTXX2_MAIZE STANDARD; PRT; 236 AA.
AC PS0472;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable glutathione S-transferase B22 (EC 2.5.1.18) (Bronze-2
DE protein).
GN B22.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Seedling;
RX MEDLINE=93005645; PubMed=1967051;
RA Nash J., Luehrens K.R., Walbot V.;
RT "Bronze-2 gene of maize: reconstruction of a wild-type allele and
RT analysis of transcription and splicing.";
RL Plant Cell 2:1039-1049(1990).
RN [2]
RP ERRATUM.
RA Nash J., Luehrens K.R., Walbot V.;
RL Plant Cell 3:103-103(1991).
CC -|- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -|- PATHWAY: Anthocyanin biosynthesis.
CC -|- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U14599; AAA50245.1; -.
DR MaizeDB; 64140; -.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.
KW Transferase.
SQ SEQUENCE 236 AA; 25563 MW; BD7C087F60FA6E9A CRC64;

Query Match 35.1%; Score 419.5; DB 1; Length 236;
Best Local Similarity 40.4%; Pred. No. 1e-26;
Matches 92; Conservative 48; Mismatches 79; Indels 9; Gaps 5;

Qy 6 LRLGAFSPALRVOIALNLKGLDYEVVEETLNP-KSELLKSNPVHKKIPVFFHG-K 63
Db 1 MRVLGVEVSPFTARLALDURGAYELLDEPLGPKSDRLAANPVYGVKIPVILLPDGR 60

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Qy 64 VICESAIIIVEYIDEVWSNNALS-----ILPQAYDRANARFWVSYYDDKWLTSLSKSVLAT 118
Db 61 AICESAVIVQYIEDVARESGAEGASLLLPDDPYERAMHREFTAFIDDKWPALDAVSLA 120
Qy 119 EDDEAKLHFEQAEVLEKVEEVFNKCSGKAYP-GGDTI-GFVDIGFGSFLSFIRVSEN 176
Db 121 PTPGARAAQAADTRAAALSLEEAFAKORSNGRAFFSGGDAAPGLDLALGCLFLPALRACER 180
Qy 177 MNERKLLDETKYGLTLWAETFAADPAVKGLLPETEKLVFAKILQK 224
Db 181 LHGLSLIDASATPLLDGWSORFAHPAARVLPDTEKRVQVQFTRFLQVQ 228

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## RESULT 3

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GTXX2_TOBAC STANDARD; PRT; 221 AA.
AC P49332;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable glutathione S-transferase parC (EC 2.5.1.18) (Auxin-regulated
DE protein parC).
GN PARC.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Xanthi NC; TISSUE=Leaf mesophyll;
RA Takahashi Y., Nagata T.;
RT "Differential expression of an auxin-regulated gene, parC, and a
RT novel related gene, C-7 from tobacco mesophyll protoplasts in
RT response to external stimuli and plant tissues.";
RL Plant Cell Physiol. 33:779-787(1992).
CC -|- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles.
CC -|- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -|- TISSUE SPECIFICITY: Abundant in seedlings and roots. It is also
CC found in the shoot tips, flowers and leaves.
CC -|- INDUCTION: By auxin.
CC -|- SIMILARITY: Belongs to the GST superfamily. Phi family.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X64398; CAA45740.1; -.
DR PIR; S19185; S19185.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferase; Multigene family.
SQ SEQUENCE 221 AA; 25743 MW; 18D27C69857EB3AE CRC64;

Query Match 34.4%; Score 410.5; DB 1; Length 221;
Best Local Similarity 41.4%; Pred. No. 5e-26;
Matches 94; Conservative 31; Mismatches 91; Indels 11; Gaps 3;

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Qy 1 MAERDLRLGAFSPALRVOIALNLKGLDYEVVEETLNPKESELLKSNPVHKKIPVFFH 60
Db 1 MANEEVLLDFWPSMFGMRRLALAEKEIKYKQEDLRNKSPLLLQNPITHKKIPVLIH 60
Qy 61 GDKVICESAIIIVEYIDEVWSNNALSILPQAYDRANARFWVSYYDDKWLTSLSKSVLAT-- 118
Db 61 NGXPICESIIAVEYIEEVWVKDKAPSLLPSPDYDRAQARFWADYIDKKLYDFGRKLWATKG 120

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QY 119 EDDAKLHPQAEVLEKVEFNKCEKAYFGCDTIGFVDFGSGFLSFIRSENMM 178
Db 121 BEQEAARKDFTECLKVLE-----GALGDRPYFGGSGFGFVDIALIGFYSWFAYETFG 173
QY 179 ERKLLDETKYGLTLWASTFAADPAVKGLLPETEKLVFAKILQIKW 225
Db 174 --NFSTEAECPKFAVAKRCMQRESVAKSLPDQPKVLEFVKVLQKPF 218

RESULT 4
GTXX4 TOBAC
ID GTXX4 TOBAC STANDARD; PRT; 221 AA.
AC Q03666;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable glutathione S-transferase (BC 2.5.1.18) (Auxin-induced protein PCNT107)
OS Nicotiana tabacum (Common tobacco)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. White Burley;
RX MEDLINE=91322513; PubMed=1863770;
RA van der Zaal E.J., Droog F.N.J., Boot C.J.M., Hengens L.A.M.,
RA Hoge J.H.C., Schilperoort R.A., Libbenga K.R.;
RT Promoters of auxin-induced genes from tobacco can lead to auxin-
RT inducible and root tip-specific expression."
RL Plant Mol. Biol. 16:983-998(1991).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- TISSUE SPECIFICITY: Root tip-specific expression.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC
CC EMBL; X56266; CAA39707.1; -
CC InterPro; IPR004046; GST_Cterm.
CC Pfam; PF00043; GST_C; 1.
CC Pfam; PF02798; GST_N; 1.
CC Transferase; MultiGene family.
CC SEQUENCE 221 AA; 25789 MW; 1488087B93BC4C60 CRC64;

Query Match 34.1%; Score 407.5; DB 1; Length 221;
Best Local Similarity 40.3%; Pred. No. 8.7e-26;
Matches 94; Conservative 29; Mismatches 87; Indels 23; Gaps 4;

QY 1 MAERDLRLGAWSPFPAIRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db 1 MANBEVILLDFWPSFGMRRLAALAEKEIKYEKEEDLNKSPLLQWNPPIHKKIPVLIIH 60
QY 61 GDKVCEIAIIVEYIDEVSNMALSILPONAYDRANARFWYSYIDDK-----WLTSL 112
Db 61 NGKPICESIIAIVEIEEVWKKAPNLLPSDYPDRAQAFWADYIDKKLYDFGRKLWTK- 119
QY 113 KSVLATEDEAKLHFEQAEVLEKVEFNKCEKAYFGCDTIGFVDFGSGFLSFIR 172
Db 120 -----GEQEAARKDFTECLKVLE-----GALGDRPYFGGSGFGFVDIALIGYSWY 167
QY 173 VSENNERKLLDETKYGLTLWASTFAADPAVKGLLPETEKLVFAKILQIKW 225
Db 168 AYETFG--NFSTEAECPKFAVAKRCMQRESVAKSLPDQPKVLEFVKVLQKPF 218

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RESULT 5
GTXX TOBAC
ID GTXX TOBAC STANDARD; PRT; 220 AA.
AC P25317;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Probable glutathione S-transferase para (EC 2.5.1.18) (Auxin-regulated protein para) (STR246C protein).
GN PARA OR PAR.
OS Nicotiana tabacum (Common tobacco)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf mesophyll;
RX MEDLINE=90083251; PubMed=2594768;
RA Takahashi Y., Kuroda H., Tanaka T., Machida Y., Takebe I., Nagata T.;
RT "Isolation of an auxin-regulated gene cDNA expressed during the
RT transition from G0 to S phase in tobacco mesophyll protoplasts.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9279-9283(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NK326;
RX MEDLINE=95036027; PubMed=7948901;
RA Froissard D., Gough C., Czernic P., Schneider M., Toppa A., Roby D.,
RA Marco Y.;
RT Structural organization of str 246C and str 246N, plant defense-
RT related genes from Nicotiana tabacum."
RL Plant Mol. Biol. 26:515-521(1994).
RN [3]
RP SEQUENCE OF 1-106 FROM N.A.
RX MEDLINE=91045927; PubMed=2236015;
RA Takahashi Y., Niwa Y., Machida Y., Nagata T.;
RT "Location of the cis-acting auxin-responsive region in the promoter
RT of the par gene from tobacco mesophyll protoplasts.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8013-8016(1990).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC
CC EMBL; D90215; BAA14243.1; -
CC EMBL; M29274; AAA67894.1; -
CC EMBL; X80829; CAA56790.1; -
CC EMBL; X80828; CAA56789.1; -
CC PIR; A36225; A36225.
CC InterPro; IPR004046; GST_Cterm.
CC InterPro; IPR004045; GST_Nterm.
CC Pfam; PF00043; GST_C; 1.
CC Pfam; PF02798; GST_N; 1.
CC Transferase; MultiGene family.
CC SEQUENCE 220 AA; 25225 MW; 2433BEA9D71D2AC8 CRC64;

Query Match 33.6%; Score 402; DB 1; Length 220;
Best Local Similarity 41.2%; Pred. No. 2.4e-25;
Matches 94; Conservative 28; Mismatches 75; Indels 18; Gaps 7;

QY 1 MAERDLRLGAWSPFPAIRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db 1 MESNNVLLDFWPSFGMRRLAALAEKEIKYEKEEDLNKSPLLLEWNPVHKKIPVLIH 60

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Qy 61 GDKVICSAAIIVEYIDVWVSNALSLPQNAVDRANARFWVSYYIDDKWLTSLKSVLA--- 117
Db 1 NSKAICSLNILEYIDVW-HDKCPLLPSDPYRSQARFWADYIDKKIYSTGRVRWSGKG 119
Qy 118 TEDDEAKLHFEQAEVLEKVE-EVFNKCSGKAYFGGDTIGFVDIGFGSFLSFIIRVSEN 176
Db 120 EDQBEAKK-----EFTILKTUEGLGN-----KTYFGGDNIGLGFVDVALVPFTSFWFSYVET 170
Qy 177 MNERKLDDETKYPGLTLWAETFAADPAVKGLLPETEKLVFAKILQK 224
Db 171 CANFSI--EAECPKLWVWAKTCMESESVSXSLPHPHKIYGF--VLELK 214

RESULT 6
GTXX ARATH
ID GTXX ARATH STANDARD; PRT; 224 AA.
AC P46421.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutathione S-transferase 103-1A (EC 2.5.1.18).
GN 103-1A OR AT2G29450 OR F16P2.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=96194465; PubMed=8624414;
RA van der Kop D.A.M., Schuyer M., Scheres B., van der Zaal B.J.,
RA Hooykaas P.J.J.;
RT "Isolation and characterization of an auxin-inducible glutathione S-
RT transferase gene of Arabidopsis thaliana.";
RL Plant Mol. Biol. 30:839-844(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX STRAIN=cv. Columbia; TISSUE=Cotyledon, and Hypocotyl;
RA Watahiki M., Yamamoto K.;
RL Submitted (XXX-1994) to the ENBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Sopory S.K.;
RT "Nucleotide sequence of glutathione S-transferase cDNA from
RT Arabidopsis thaliana.";
RL Submitted (APR-1999) to the ENBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnes M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC -----
DR EMBL; X89216; CAA61504.1; -.
DR EMBL; U30489; AAA74019.1; -.
DR EMBL; D44465; BAA07917.1; -.
DR EMBL; AF144382; AAD34992.1; -.
DR EMBL; AC004561; AAC95193.1; -.
DR PIR; S66354; S66354.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR Transferrase.
KW SEQUENCE 224 AA; 26000 MW; BA2F5C06B94FFCC4 CRC64;

Query Match 33.4%; Score 399; DB 1; Length 224;
Best Local Similarity 41.1%; Pred. No. 4.3e-25;
Matches 90; Conservative 39; Mismatches 80; Indels 10; Gaps 5;

Qy 1 MAER-DLRLGAWFSPALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFF 59
Db 1 MAEKEEVKLLGIWASPFRRVEMALKLGIPYEYVEILENKSPLLALNPIHKKVPLV 60
Qy 60 HGDKVICSAAIIVEYIDVWVSNALSLPQNAVDRANARFWVSYYIDDKWLTSLKSVLATE 119
Db 61 HNGKTLSEHVILEYIDETWPQN--PLPQDPYRSQARFWADYIDKKIYSTGRVRWSGKG 118
Qy 120 DDEAKLHFEQAEVLEKVEFNKCSGKAYFGGDTIGFVDIGFGSFLSFI--RVSEN 177
Db 119 DEKREVLAEQVRELIMYLE----KELVGKDYFGGKTVGLDFVAGSLIPFCLERGWEG 174
Qy 178 NERKLDDETKYPGLTLWAETFAADPAVKGLLPETEKLV 216
Db 175 G-LEVITEEFEPFKRWVRNLEKVEIVKDCVPPREHVE 212

RESULT 7
GTXX TOBAC
ID GTXX TOBAC STANDARD; PRT; 223 AA.
AC Q03662;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable glutathione S-transferase (EC 2.5.1.18) (Auxin-induced
DE protein PGNT1/PCNT110).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamnids; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. White Burley, and cv. Samsun NN; TISSUE=Leaf;
RX MEDLINE=91322513; PubMed=1863770;
RA van der Zaal E.J., Droog F.N.J., Boot C.J.M., Hensgens L.A.M.,
RA Hoge J.H.C., Schilperoort R.A., Libbenga K.R.;
RT "Promoters of auxin-induced genes from tobacco can lead to auxin-
RT inducible and root tip-specific expression.";
RL Plant Mol. Biol. 16:983-998(1991).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- TISSUE SPECIFICITY: Root tip-specific expression.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC
DR EMBL; X56268; CAA39709.1; -.
DR EMBL; X56264; CAA39705.1; -.

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Query Match 31.6%; Score 378; DB 1; Length 219;  
Best Local Similarity 39.7%; Pred. No. 2e-23;  
Matches 92; Conservative 28; Mismatches 78; Indels 34; Gaps 6

QY 8 LIGAWFSPALRVQIALNLKGLDYEVEVETLNPKEKLLKSNPVHKKIPVFFHGDVCE 67  
DB 7 LDTWASMYGMRARIALAEGVRYEKEENLNMRSPLLQMMPIHKKIPVLIHNGKPICE 66

QY 68 SAIIVEYIDEVMSNALSILPQNAVDRANARFWSYIDDK-----WLTSLSKSVLATE 119  
DB 67 SAIIVQYIDEVW-NDKSPMLPSDPYKRSQARFWDYIDDKIYDTWKQWLSK-----GSE 120

QY 120 DDEAKK---LHFQAEAEVLEKVEEVFNKCEKAVFGDGTIGFVDIGFSGFSFTRVSEN 176  
DB 121 HEBGKELISIFKQLEETL-----TDKPFYGDGTGFGVLDCLITFFSWFYET 169

QY 177 MNERKLLDTEKYPGLTMAETFAADPAVKGLLPETEK---LVEFAKILQLX 224  
DB 170 YGNFKM---EECPKLMWVKRCMERETVNTLPDAKKYGLIVELQKLTESK 219

RESULT 9  
GT2X\_TOBAC  
ID GT2X\_TOBAC STANDARD; PRT; 223 AA.  
AC QX3663;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Probable glutathione S-transferase (EC 2.5.1.18) (Auxin-induced protein PGN735/PCNT11).  
DE Nicotiana tabacum (Common tobacco).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. White Burley, and cv. Samsun NN; TISSUE=Leaf;  
RC MEDLINE=91322513; PubMed=1863770;  
RA van der Zaal E.J., Droog F.N.J., Boot C.J.M., Hengens L.A.M.,  
RA Hoge J.H.C., Schiperoort R.A., Libbenga K.R.;  
RT "Promoters of auxin-induced genes from tobacco can lead to auxin-inducible and root tip-specific expression";  
RL Plant Mol. Biol. 16:983-998(1991).  
CC -/- CATALYTIC ACTIVITY: RX + Glutathione = HX + R-S-glutathione.  
CC -/- TISSUE SPECIFICITY: Root tip-specific expression.  
CC -/- INDUCTION: By auxin.  
CC -/- SIMILARITY: Belongs to the GST superfamily. HSP26 family.

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CC ENBL; X56269; CAA39710.1; -  
CC ENBL; X56285; CAA39706.1; -  
CC PIR; S16268; S16288.  
CC InterPro; IPR004046; GST\_Cterm.  
CC InterPro; IPR004045; GST\_Nterm.  
CC Pfam; PF00043; GST\_C; 1.  
CC Pfam; PF02798; GST\_N; 1.  
KW Transferase; Multigene family.  
SQ SEQUENCE 223 AA; 25841 MW; ACD523DB2A03A83 CRC64;

Query Match 31.3%; Score 373.5; DB 1; Length 223;  
Best Local Similarity 37.9%; Pred. No. 4.8e-23;  
Matches 88; Conservative 46; Mismatches 85; Indels 13; Gaps 6

QY 1 MAERDURLLGAWFSPALRVQIALNLKGLDYEVEVETLNPKEKLLKSNPVHKKIPVFFH 60

Query Match 32.0%; Score 392; DB 1; Length 223;  
Best Local Similarity 39.0%; Pred. No. 1.6e-24;  
Matches 90; Conservative 43; Mismatches 88; Indels 10; Gaps 4;

QY 1 MAERDURLLGAWFSPALRVQIALNLKGLDYEVEVETLNPKEKLLKSNPVHKKIPVFFH 60  
DB 1 MAE---VKLLGFWYSPFREVWALKIKGVYIEIEDRDNKSSLLQSNPIHKKVPLVLIH 58

QY 61 GDKVICSALIVEYIDEVMSNALSILPQNAVDRANARFWSYIDDKWLTSLSKSVLATE 120  
DB 59 NGRKIVESWVILEYIDETEGP---SILPKDPYDALARFWAKFLDDKVPVVKTLRKE 116

QY 121 DEAKKLHFRQAEVLEKVEEVFNKCEKAVFGDGTIGFVDIGFSGFSFTRVSENMMNER 180  
DB 117 EQEKK-----DKEVCEMLKVLNDELK-KKPFVGDGFGFADIAANLVAFLGVFEASGV 170

QY 181 KLLDTEKYPGLTMAETFAADPAVKGLLPETEKVFAKILQLKWAASAAA 231  
DB 171 VLVTSKFPNFKWGRGEYINCISQIKESLPPRDELLAFYRSQAAAASASA 221

RESULT 8  
LGUL\_SOYBN  
ID LGUL\_SOYBN STANDARD; PRT; 219 AA.  
AC P46417;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase)  
DE (Aldoketomutase) (Glyoxalase I).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RC Koellner B., Finkelnburg B., Mayerbacher R., Paulus C.,  
RA Springer B.;  
RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.  
CC -/- FUNCTION: Catalyzes the conversion of hemimercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione.  
CC -/- CATALYTIC ACTIVITY: (R)-S-lactoylglutathione = glutathione + methylglyoxal.  
CC -/- PATHWAY: Glyoxal pathway.  
CC -/- SIMILARITY: Belongs to the GST superfamily. HSP26 family.

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CC ENBL; X68819; CAA48717.1; -  
CC PIR; S47177; S47177.  
CC InterPro; IPR004046; GST\_Cterm.  
CC InterPro; IPR004045; GST\_Nterm.  
CC Pfam; PF00043; GST\_C; 1.  
CC Pfam; PF02798; GST\_N; 1.  
KW Lyase.  
SQ SEQUENCE 219 AA; 25901 MW; 6A2E46B759476A8C CRC64;

```
Db 1 MAE--VKLLGFWSPPSHRVEWALKIKGVKVEYTEEDRDNKSSLLQSNPVYKVPVLIIH 58
Qy 61 GDKVICSATIVVEYIDVWSNNALSILPONAYDRANARFWWSYIDDKWLTSLSKSVLATED 120
Db 59 NGKPIVESMIILEYIDTFEGP--SILPKOPYDRALARFAWAKFLDDK-VAADVNTTFRKG 115
Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGDGTIGFVDIGRGSFLSFRVSENMMNER 180
Db 116 EOEK----GKEEYEMLKVLDELKD-KKFFAGDKFGFADIAANLVGFWLGVFEYGYD 170
Qy 181 KLDETKYPGTLTWAETFAADPAVKGLLPETEKLEVEPAKI-LQKWAASAAK 232
Db 171 VLKSEKFPNFKWRDYEYINCSQVNESLPPRDELLAF---FRARQAVVASR 219

RESULT 10
GTXL_SOLTU
ID _GTXL_SOLTU STANDARD; PRT; 217 AA.
AC Q32111;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable glutathione S-transferase (EC 2.5.1.18) (Pathogenesis-related protein 1).
GN PRP1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92063197; PubMed=2132026;
RA Taylor J.L., Fritzenmeier K.H., Heuser I., Kombrink E., Rohwer F.,
RA Schroeder M., Srittmater G., Hahlbrock K.;
RT "Structural analysis and activation by fungal infection of a gene
RT encoding a pathogenesis-related protein in potato.";
RL Mol. Plant Microbe Interact. 3:72-77(1990).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- INDUCTION: By fungal infection.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J03679; AAA68430.1; -.
DR PIR; T07595; T07595.
DR InterPro; IPR004046; GST_Cterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Plant defense; Transferase; Pathogenesis-related protein.
SQ SEQUENCE 217 AA; 25056 MW; 7B0DBBE216685B4E CRC64;

Query Match 31.1%; Score 372; DB 1; Length 217;
Best Local Similarity 41.4%; Pred. No. 6.1e-23;
Matches 82; Conservative 35; Mismatches 71; Indels 10; Gaps 4;

Qy 1 MAERDLRLGAWSPFALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db 1 MAE--VKLLGLRYGPFSSHRVEWALKIKGVKVEYTEEDLQNKSPLLQSNPIHKKIPVLIIH 58
Qy 61 GDKVICSATIVVEYIDVWSNNALSILPONAYDRANARFWWSYIDDKWLTSLSKSVLATED 120
Db 59 NGKPIVESMIILEYIDTFEGP--SILPKOPYDRALARFAWAKFLDDK-VAADVNTTFRKG 115
Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGDGTIGFVDIGRGSFLSFRVSENMMNER 180
Db 171 VLKSEKFPNFKWRDYEYINCSQVNESLPPRDELLAF---FRARQAVVASR 219

RESULT 11
GTXL3_TOBAC
ID _GTXL3_TOBAC STANDARD; PRT; 223 AA.
AC Q03664;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Probable glutathione S-transferase (EC 2.5.1.18) (Auxin-induced protein PCNT103).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. White Burley;
RX MEDLINE=91322513; PubMed=1863770;
RA van der Zaal E.J., Droog F.N.J., Boot C.J.M., Hensgens L.A.M.,
RA Hoge J.H.C., Schilperoort R.A., Libbenga K.R.;
RT "Promoters of auxin-induced genes from tobacco can lead to auxin-
RT inducible and root tip-specific expression.";
RL Plant Mol. Biol. 16:983-998(1991).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- TISSUE SPECIFICITY: Root tip-specific expression.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X56263; CAA39704.1; -.
DR PIR; S16269; S16269.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferase; MultiGene family.
SQ SEQUENCE 223 AA; 25747 MW; 22CD25BB5A05D214 CRC64;

Query Match 31.1%; Score 371.5; DB 1; Length 223;
Best Local Similarity 39.1%; Pred. No. 6.9e-23;
Matches 91; Conservative 42; Mismatches 89; Indels 11; Gaps 6;

Qy 1 MAERDLRLGAWSPFALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db 1 MAE--VKLLGFWSPPSHRVEWALKIKGVKVEYTEEDRDNKSSLLQSNPVYKVPVLIIH 58
Qy 61 GDKVICSATIVVEYIDVWSNNALSILPONAYDRANARFWWSYIDDKWLTSLSKSVLATED 120
Db 59 NGKPIVESMIILEYIDTFEGP--SILPKOPYDRALARFAWAKFLDDK-VAADVNTTFRKG 115
Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGDGTIGFVDIGRGSFLSFRVSENMMNER 180
Db 116 EOEK----GKEEYEMLKVLDELKD-KKFFAGDKFGFADIAANLVGFWLGVFEYGYV 170
Qy 181 KLDETKYPGTLTWAETFAADPAVKGLLPETEKLEVEPAKI-LQKWAASAAK 232
Db 171 VLKSEKFPNFKWRDYEYINCSQVNESLPPRDELLAF---FRARQAVVASISAPK 223
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Db 117 EOEKAK--BEAYEMLKILDNEF-----KDKKCFVGDKFGFADIVANGAALYLGIILEVSGI 170
Qy 181 KLDETKYPGTLTWAETTF 198
Db 171 VLATSEKFPNFCAMRDEY 188

RESULT 11
GTXL3_TOBAC
ID _GTXL3_TOBAC STANDARD; PRT; 223 AA.
AC Q03664;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Probable glutathione S-transferase (EC 2.5.1.18) (Auxin-induced protein PCNT103).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. White Burley;
RX MEDLINE=91322513; PubMed=1863770;
RA van der Zaal E.J., Droog F.N.J., Boot C.J.M., Hensgens L.A.M.,
RA Hoge J.H.C., Schilperoort R.A., Libbenga K.R.;
RT "Promoters of auxin-induced genes from tobacco can lead to auxin-
RT inducible and root tip-specific expression.";
RL Plant Mol. Biol. 16:983-998(1991).
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -!- TISSUE SPECIFICITY: Root tip-specific expression.
CC -!- INDUCTION: By auxin.
CC -!- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC
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CC
CC EMBL; X56263; CAA39704.1; -.
DR PIR; S16269; S16269.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferase; MultiGene family.
SQ SEQUENCE 223 AA; 25747 MW; 22CD25BB5A05D214 CRC64;

Query Match 31.1%; Score 371.5; DB 1; Length 223;
Best Local Similarity 39.1%; Pred. No. 6.9e-23;
Matches 91; Conservative 42; Mismatches 89; Indels 11; Gaps 6;

Qy 1 MAERDLRLGAWSPFALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
Db 1 MAE--VKLLGFWSPPSHRVEWALKIKGVKVEYTEEDRDNKSSLLQSNPVYKVPVLIIH 58
Qy 61 GDKVICSATIVVEYIDVWSNNALSILPONAYDRANARFWWSYIDDKWLTSLSKSVLATED 120
Db 59 NGKPIVESMIILEYIDTFEGP--SILPKOPYDRALARFAWAKFLDDK-VAADVNTTFRKG 115
Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGDGTIGFVDIGRGSFLSFRVSENMMNER 180
Db 116 EOEK----GKEEYEMLKVLDELKD-KKFFAGDKFGFADIAANLVGFWLGVFEYGYV 170
Qy 181 KLDETKYPGTLTWAETFAADPAVKGLLPETEKLEVEPAKI-LQKWAASAAK 232
Db 171 VLKSEKFPNFKWRDYEYINCSQVNESLPPRDELLAF---FRARQAVVASISAPK 223
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RESULT 12
GTXX1_NICPL STANDARD; PRT; 219 AA.
AC P50471;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable glutathione S-transferase MSR-1 (EC 2.5.1.18) (Auxin-
regulated protein MSR-1).
GN MSR-1.
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92361262; PubMed=1498603;
RA Dominov J.A., Stenzler L., Lee S., Schwarz J.J., Leisner S.,
RA Howell S.H.;
RT "Cytokinin and auxins control the expression of a gene in Nicotiana
plumbaginifolia cells by feedback regulation.";
RL Plant Cell 4:451-461(1992).
CC -I- FUNCTION: May play an important role in hormonal and growth
regulatory responses.
CC -I- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -I- INDUCTION: By auxin and cytokinin.
CC -I- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC -----
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CC -----
DR EMBL; S44036; AAB47712.2; -.
DR PIR; JQ1606; JQ1606.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
DR Transferase; 129 129 GLY-RICH.
KW TRANSFERASE; Multigene family.
SQ SEQUENCE 219 AA; 25269 MW; DCE165B0FB33A759 CRC64;

Query Match 30.3%; Score 361.5; DB 1; Length 219;
Best Local Similarity 39.0%; Pred. No. 4.3e-22;
Matches 89; Conservative 35; Mismatches 85; Indels 19; Gaps 7;

QY 1 MAERDLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
DB 1 MESNNVLLDPSGSGFGRRLIALALGKYEAKENLSDKSPLLLEWNPVHKKIPILIH 60
QY 61 GDKVCSAIIIVEYIDEVWNSNLSILPQAYDANARFVSYDDKWLISLKSVLATED 120
DB 61 NGKPICESNLILEYIDEVW-HEKCLLPSPDYQSQARFANYIDNKIYSTGRVSGKG 119
QY 121 DEAKKLHFEQAEVLEVKVEEVFNKCSG- ---KAYFGSDTIGFVDIGFGSFLSPIRVSEN 176
DB 120 -----EQDEEAKKGFIETF-KTLEGLGNKTYFGDNLGDFVDVALVPTSFYSYET 170
QY 177 MNERKLDDETKYPGLTWAETFAADPAVKGGLLPETEKLVFEPAKILQLK 224
DB 171 CANFSI--EASCRKLWQNCWENERSVSKS-LPHPKIYDF--VLELK 213

RESULT 13
GTXXC_ORYSA STANDARD; PRT; 254 AA.
AC Q06398;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

QY 01-NOV-1995 (Rel. 32, Last annotation update)
DE Probable glutathione S-transferase (EC 2.5.1.18) (28 kDa cold-induced
protein).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare; TISSUE=Seedling;
RA Binh L.T., Oono K.;
RT "Molecular cloning and characterization of genes related to
chilling tolerance in rice.";
RL Plant Physiol. 99:1146-1150(1992).
CC -I- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -I- TISSUE SPECIFICITY: Seedling shoots and roots.
CC -I- SIMILARITY: Belongs to the GST superfamily. HSP26 family.
CC -----
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CC -----
DR EMBL; D10861; BAA01632.1; -.
DR Gramene; Q06398; -.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.
KW TRANSFERASE.
FT DOMAIN 121 129 GLY-RICH.
FT DOMAIN 158 168 ARG-RICH.
SQ SEQUENCE 254 AA; 28241 MW; 8D3FD11AAA782A8F CRC64;

Query Match 17.0%; Score 203.5; DB 1; Length 254;
Best Local Similarity 44.7%; Pred. No. 2.6e-09;
Matches 42; Conservative 17; Mismatches 30; Indels 5; Gaps 2;

QY 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHG--- 61
DB 6 ELKLLGWSSPYAIRVRLNLKSLPYEVEENLGDKDLLASNPVHKSVPVLLHAGRR 65
QY 62 DKVICSAAIIVEYIDEVWNSNLSILPQAYDRA 95
DB 66 ERVAGHRAVHRGL--AGARRGRSVMPSDPYERA 97

RESULT 14
GTOL_PIG STANDARD; PRT; 241 AA.
AC Q2N1F5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutathione transferase omega 1 (EC 2.5.1.18) (GSTO 1-1) (Glutathione-
dependent dehydroascorbate reductase).
GN GSTO1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 5-31; 58-83; 101-110; 115-147;
RP 149-160; 162-190; 201-228 AND 235-241, SUBUNIT, SUBCELLULAR LOCATION,
RP TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Liver;
RX MEDLINE=21378194; PubMed=11485575;
RA Rouimi P., Anglade P., Benzekri A., Costet P., Debrauer L.,
RA Pineau T., Tulliez J.;
RT "Purification and characterization of a glutathione S-transferase
Omega in pig: evidence for two distinct organ-specific transcripts.";
```





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OM protein - protein search, using sw model

Run on: October 8, 2004, 09:16:45 ; Search time 39 Seconds  
(without alignments)  
572.216 Million cell updates/sec

Title: US-10-088-945A-10  
Perfect score: 1195  
Sequence: 1 MAERDLRLGAWFSPFALRV.....KLVEFAKILQKWAARAAK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	49.9	234	2 F96620	hypothetical prote
2	558	46.7	233	2 D96620	protein T30E16.25
3	520	43.5	470	2 H86397	protein T7N9.20 [i
4	491.5	41.1	234	2 G96721	probable glutathio
5	486.5	40.7	229	2 F96721	probable glutathio
6	429.5	35.9	225	2 A33654	heat shock protein
7	426	35.6	224	2 A84637	probable glutathio
8	412.5	34.5	241	2 S22457	Bronze-2 protein -
9	411	34.4	230	2 T10825	auxin-induced prot
10	410.5	34.4	221	2 S19185	parC protein - com
11	407.5	34.1	221	2 S16636	auxin-induced prot
12	403	33.7	161	2 T09807	probable glutathio
13	402	33.6	220	2 A36225	auxin-regulated pr
14	399	33.4	224	2 S66354	glutathione transf
15	397.5	33.3	225	2 G84696	probable glutathio
16	396.5	33.2	218	2 T09781	glutathione transf
17	394	33.0	219	2 T06239	probable glutathio
18	392	32.8	223	2 S16272	auxin-induced prot
19	390	32.6	216	2 T07156	probable glutathio
20	383.5	32.1	225	2 H84696	probable glutathio
21	378	31.6	219	2 S47177	lactoylglutathione
22	377	31.5	224	2 F84696	probable glutathio
23	376	31.5	220	2 A86308	probable glutathio
24	373.5	31.3	223	2 S16268	auxin-induced prot
25	372.5	31.2	227	2 B84696	probable glutathio
26	372	31.1	217	2 T07595	glutathione transf
27	371.5	31.1	223	2 S16269	auxin-induced prot
28	371	31.0	220	2 C96812	protein F3F9.14 [i
29	371	31.0	223	2 D84696	probable glutathio

30	371	31.0	224	2 T12332	glutathione transf
31	365	30.5	224	2 T04358	glutathione transf
32	364	30.5	219	2 T51607	glutathione transf
33	361.5	30.3	219	2 JQ1606	multiple stimulus
34	361	30.2	224	2 A96577	probable glutathio
35	359	30.0	218	2 G86307	probable glutathio
36	357.5	29.9	219	2 S19182	gene C-7 protein -
37	353.5	29.6	221	2 H86307	probable glutathio
38	318	26.6	232	2 A96775	probable glutathio
39	317	26.5	227	2 T47416	glutathione transf
40	307	25.7	231	2 T02765	glutathione transf
41	204	17.1	102	2 F86237	protein F14N23.25
42	180.5	15.1	257	2 S33114	beta-etherase ligf
43	170.5	14.3	266	2 T20806	hypothetical prote
44	164	13.7	213	2 T06333	probable glutathio
45	164	13.7	220	2 S33628	glutathione transf

ALIGNMENTS

RESULT 1

F96620  
hypothetical protein F23H11.1 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: F96620  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federespiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: F96620  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-234 <STO>  
A;Cross-references: GB:AE005173; NID:g5080803; PIDN:AAD39312.1; GSPDB:GN00141  
C;Genetics:

A;Gene: F23H11.1  
A;Map position: 1  
C;Superfamily: auxin-induced protein  
Query Match 49.9%; Score 596; DB 2; Length 234;  
Best Local Similarity 49.6%; Pred. No. 3.6e-41;  
Matches 115; Conservative 46; Mismatches 69; Indels 2; Gaps 2;  
Qy 1 MAER-DLRLGAWFSPFALRVQIALNLKGDYVEVETL-NPKSELLKGNPHVKIPVF 58  
Db 1 MGKEEVKLLGVWYSPVAPRKIALRKSDYDYVEENLFGSKSELLKGNPHVKIPVL 60  
Qy 59 FHGDKVCEAAIIVEYIDEVMSNNALSPQNYADRANARFWVSYYDDKMLTSLKSVLAT 118  
Db 61 LHNNKPIVESLNIVEYIDETWSSAPSLPSHPYDRALARFWSDFVDNKNFPALRMAAIT 120  
Qy 119 EDDEAKLHFEQAEVELEKVEEVNKCSEKAYFGGTIGFVDIGFSGFLSFIRVSENMN 178  
Db 121 KSEDAKAKAEVEVEGLQLQEDAFVSIKSGKPPFGGSAIGFMDICFGFVLLKAREKFK 180  
Qy 179 ERKLDETQVPGTLTWAETFAADPAVKGLLPETEKLVFAKILQLKWAARAAA 230  
Db 181 AEKLLDESKTPSLCKWADRFLSDETVKNVAPEIEKVAEFLQEVRAQSAAS 232

RESULT 2

D96620  
protein T30E16.25 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: D96620  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzb, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
C;Accession: D96620  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <STO>  
A;Cross-references: GB:AE005173; NID:g8778750; PIDN:AAF79758.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: T30E16.25  
A;Map position: 1  
C;Superfamily: auxin-induced protein

Query Match 46.7%; Score 558; DB 2; Length 233;  
Best Local Similarity 48.4%; Pred. No. 4.4e-38;  
Matches 106; Conservative 42; Mismatches 69; Indels 2; Gaps 2;

Qy 1 MAER-DRLGAWFSPFALRVQIALNLKGLDYEVVEE-L-NPKSELLKSNPVHKKIPV 58  
Db 1 MGEEREVKLLTSSPPVIRAKIALRUKSDYDVEEDLFGSKSELLKSNPIPKKPVVL 60

Qy 59 FHGDKVCSAIIVEYIDVWNNALSILPONAYDRANARFWVSYYDDKWLTSLSKVLAT 118  
Db 61 IHNTKPCVSLNIVEYIDETWSSGSSILPSPHYDRALARFWVSFVDDKWLPTLMAAVVA 120

Qy 119 EDDBAKLLHFEQAEVLEKVEEVNFKSCGKAYFGGDTIGFVDIGFSGFSFIRVSENMN 178  
Db 121 KSEBAKAGMBEVEGLQLAEAFALSKGKSFSGGTIGFIDICLSFLVLKAREKJK 180

Qy 179 ERKLLDETKYPGTLTWAETFAADPAVKGLLPETKLVF 217  
Db 181 NEKILDELKTPSLRYWANQFLSNENWVNVDPIDKVKF 219

RESULT 3  
H86397  
protein T7N9.20 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: H86397  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzb, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
C;Accession: H86397  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-470 <STO>  
A;Cross-references: GB:AE005172; NID:g8778860; PIDN:AAF79859.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: T7N9.20  
A;Map position: 1

Query Match 43.5%; Score 520; DB 2; Length 470;  
Best Local Similarity 47.7%; Pred. No. 1.3e-34;  
Matches 106; Conservative 39; Mismatches 73; Indels 4; Gaps 3;

Qy 1 MAER-DRLGAWFSPFALRVQIALNLKGLDYEVVEE--TLNPKSELLKSNPVHKKIPV 57  
Db 1 MAQNDTIVKLTGSSNPSYSLRARVALHLKSVKYEYLDPEPDLKESKSELLKSNPIHKKVPV 60

Qy 58 FHGDKVCSAIIVEYIDVWNNALSILPONAYDRANARFWVSYYDDKWLTSLSKVL 117  
Db 61 LRGDLSISSESLNVQVVDRAWP-SVPSILPSDAYDRASARFWAQYIDDKCFRAADVAVG 119

Qy 118 TEDEAKLLHFEQAEVLEKVEEVNFKSCGKAYFGGDTIGFVDIGFSGFSFIRVSEN 177  
Db 120 AKDDEGMAAVKLMCLALETFQKSSKGLGFFGGETIGYLDIACALLGPISVIEAF 179

Qy 178 NERKLLDETKYPGTLTWAETFAADPAVKGLLPETKLVF 219  
Db 180 SGVKFLRQETTPGLIKWAERFRAHEAVKPYMPTVEEVVAF 221

RESULT 4  
G96721  
probable glutathione transferase T17F3.4 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: G96721  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzb, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
C;Accession: G96721  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-234 <STO>  
A;Cross-references: GB:AE005173; NID:g6358801; PIDN:AAF07381.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: T17F3.4  
A;Map position: 1  
C;Superfamily: auxin-induced protein

Query Match 41.1%; Score 491.5; DB 2; Length 234;  
Best Local Similarity 46.0%; Pred. No. 1.1e-32;  
Matches 99; Conservative 36; Mismatches 79; Indels 1; Gaps 1;

Qy 6 LRLGAWFSPFALRVQIALNLKGLDYEVVEE-L-NPKSELLKSNPVHKKIPVFFHGDV 65  
Db 13 VKLLGAWFSPFVLKTRIALNLKNVAVYLEEEDTLSSSEVLNVPVHVKQIPILHGNKPI 72

Qy 66 CSAIIVEYIDVWNNALSILPONAYDRANARFWVSYYDDKWLTSLSKVLATDEDAKK 125  
Db 73 RESLNIYMYDVTWLSGP-PILSPDPFRAVARPDVYIDHCFTSINGVAVAGENIN 131

Qy 126 LHFEQAEVLEKVEEVNFKSCGKAYFGGDTIGFVDIGFSGFSFIRVSENMRKLLDE 185  
Db 132 AATAKLEQCWALLLEETQECCKGKGFGENIGFIDIGFSGMLGPLVLEKFTGVKFIHP 191

Qy 186 TKYPGLTWAETFAADPAVKGLLPETKLVF 220  
Db 192 ENTPGLFHMDRFFVAHEAVKPVMPDIEKLQVAF 226

RESULT 5  
F96721  
probable glutathione transferase T17F3.5 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C;Accession: F96721  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rozeberg, S.L.; Rowley, D.; Sakano, H.  
C;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: F96721  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-229 <STO>  
A;Cross-references: GB:AE005173; NID:96358802; PIDN:AAF07382.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: T17F3.5  
A;Map position: 1  
C;Superfamily: auxin-induced protein

Query Match 40.7%; Score 486.5; DB 2; Length 229;  
Best Local Similarity 47.2%; Pred. No. 2.8e-32;  
Matches 102; Conservative 33; Mismatches 78; Indels 3; Gaps 2;

Qy 6 LRLGAWFSPALRVQIALNKLGLDYEVVEET--LNPKESELLKSNPVHKKIPVFFHGD 63  
Db 10 VKLGTWASPPAIRAQVALHUKSVHEHYVEETDLVKGKSDLLIKSNPIHKKVPVLIHGDV 69

Qy 64 VICSAIIVEYIDEVWNNALSIIPQAYDRANARFWVSYYDDKWLTSLSKVLATDEDA 123  
Db 70 SICESLNIQVDESWSFD--LSILPTLPSERAFARFAHFDVGLKFSIDAVAGAKDDAA 128

Qy 124 KGLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFSGFLSFIRVSENNNERKLL 183  
Db 129 RMTLAGNLMLAALAEAFQKSKGDFGFGGNTGFDITVGAIVGPISVIEAFSGVKFL 188

Qy 184 DETKYRGLTWAETFAADPAVKGLLPETEKLEVEAK 219  
Db 189 RPDTPGLIOWAEKFAHEAVKPYMTVAEPIEPAK 224

RESULT 6  
A33654  
heat shock protein 26A - soybean  
C;Species: Glycine max (soybean)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 17-Nov-2000  
C;Accession: A33654; A28662  
R;Czarnecka, E.; Nagao, R.T.; Key, J.L.; Gurley, W.B.  
Mol. Cell. Biol. 8, 1113-1122, 1988  
A;Title: Characterization of Gmhs26-A, a stress gene encoding a divergent heat shock pr  
A;Reference number: A33654; MUID:88216585; PMID:2835661  
A;Accession: A33654  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-225 <CZA>  
A;Cross-references: GB:M20363; NID:g169980; PIDN:AAA33973.1; PID:g169981  
R;Hagen, G.; Uhrhammer, N.; Guilfoyle, T.J.  
J. Biol. Chem. 263, 6442-6446, 1988  
A;Title: Regulation of expression of an auxin-induced soybean sequence by cadmium.  
A;Reference number: A28662; MUID:88198196; PMID:3360788  
A;Accession: A28662  
A;Molecule type: mRNA  
A;Residues: 86-225 <HAG>  
C;Genetics:  
A;Introns: 107/3  
C;Superfamily: auxin-induced protein

Query Match 35.9%; Score 429.5; DB 2; Length 225;  
Best Local Similarity 40.7%; Pred. No. 1.2e-27;  
Matches 94; Conservative 46; Mismatches 80; Indels 11; Gaps 5;

Qy 3 ERDRLGAWFSPALRVQIALNKLGLDYEVVEETLNPKESELLKSNPVHKKIPVFFHGD 62  
Db 10 VKLGTWASPPAIRAQVALHUKSVHEHYVEETDLVKGKSDLLIKSNPIHKKVPVLIHGDV 69

Db 5 QEDVKLLGIVGSPFCRVQIALNKLGVYKYLEENLGNKSDLLKYNPVHKKVPVFFVHNE 64  
Qy 63 KVTCESAIIVEYIDEVWNNALSIIPQAYDRANARFWVSYYDDKWLTSLSKVLATDEDD 122  
Db 65 QPIAESLIVIVEYIDETWKN--PILPSDPYQALAREWKFIDDKIYGAWSKVSFTVDEK 122  
Qy 123 AKKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFSGFLSF--IRVSENMMERK 181  
Db 123 ERKNVEETEAALQFLENEI----KDKKFGGSEFGLVDIA-AVFIAPWIPFQEIAGLQ 177  
Qy 182 LLDETKYRGLTWAETFAADPAVKGLLPETEKLEVEFAKILQLKWAANAAAK 232  
Db 178 LFTSEKFPILYKWSQSFNLHPFVHVLPRDPLFAVEK---ARVESLSASK 225

RESULT 7  
A84697  
probable glutathione S-transferase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C;Accession: A84697  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: A84697  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-224 <STO>  
A;Cross-references: GB:AE002093; NID:g3980386; PIDN:AAC95189.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g29490  
A;Map position: 2  
C;Superfamily: auxin-induced protein

Query Match 35.6%; Score 426; DB 2; Length 224;  
Best Local Similarity 42.1%; Pred. No. 2.2e-27;  
Matches 93; Conservative 48; Mismatches 66; Indels 14; Gaps 7;

Qy 1 MAERD--LRLGAWFSPALRVQIALNKLGLDYEVVEETLNPKESELLKSNPVHKKIPV 58  
Db 1 MAEKESVRLGLGFASPFSSRVEMALKLGVPYELEDLPNKTPLLELNLPHKKVPVL 60

Qy 59 FHGDKVICSIAIIVEYIDEVWNNALSIIPQAYDRANARFWVSYYDDKWLTSLSKSLA 117  
Db 61 VHNDKILLESLLILEYIDQWKN--PILQDPYKAMARFAKFIQDQILTLGFRSLVK 118

Qy 118 TEDEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFSGFLSF--IRVSE 175  
Db 119 AE--KGEVAIEETRELLMFLE----KEVTGKDFGKGTIGFLDMTAGSMIPFCLARLWK 172

Qy 176 NMNERKLLDETYPGLTWAETFAADPAVKGLLPETEKLEVE 216  
Db 173 GIG-IDMPEKPELNRWIKNLEEVAVRGCIIPPEKQIE 212

## RESULT 8

S22457

Bronze-2 protein - maize

C;Species: Zea mays (maize)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999

C;Accession: S22457; JQ0987; S58414

R;Schmitz, G.; Theres, K.

Mol. Gen. Genet. 233, 269-277, 1992

A;Title: Structural and functional analysis of the Bz2 locus of Zea mays: characterizati

A;Reference number: S22457; MUID:92293125; PMID:1376405

A;Accession: S22457

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-241 &lt;SCH&gt;

R;Nash, J.; Luehrs, K.R.; Walbot, V.

Plant Cell 2, 1039-1049, 1990  
A;Title: Bronze-2 gene of maize: reconstruction of a wild-type allele and analysis of the  
A;Reference number: JQ0987; MUID:93005645; PMID:1967051  
A;Accession: JQ0987  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-195,198-233,'VO',234-241 <NAS>  
R;Marrs, K.A.; Alfinito, M.R.; Lloyd, A.M.; Walbot, V.  
Nature 375, 397-400, 1995  
A;Title: A glutathione S-transferase involved in vacuolar transfer encoded by the maize  
A;Reference number: S58414; MUID:95281051; PMID:7760932  
A;Contents: annotation  
C;Genetics:  
A;Gene: Bz2  
A;Introns: 114/3  
C;Function:  
A;Description: required for production of anthocyanin pigment  
A;Pathway: anthocyanin biosynthesis  
C;Superfamily: auxin-induced protein

Query Match 34.5%; Score 412.5; DB 2; Length 241;  
Best Local Similarity 39.8%; Pred. No. 3.1e-26;  
Matches 94; Conservative 47; Mismatches 84; Indels 11; Gaps 6;

Qy 1 MAERDLRLGAWSPFPALRVQIALNLKGLDYEVVEETLNP-KSELLLLKSNPVHKKIPVFF 59  
Db 1 MTAGTMRVLGGEVSPFTARARLALDLRGVAYELDELPLGPKSDRLAANPVYKIPVLL 60

Qy 60 HGD-KVICESAIIVEYIDEVWSNNALS-----ILPQAYDRANARFWVSVIDDKWLSLK 113  
Db 61 LPDGRAICESAVIQYIEDVARESGBAGSLLPLDPFYERAMRFWTAFIDDKFEPALD 120

Qy 114 SVLATEDDEAKLHFEQAEVLEKVEVFNKCSGKAYF-GGDYI-GFVDIGFGSFLSFI 171  
Db 121 AVSLAPFGARAQAEADTRALSILEAFKDRSNGRAFFSGGDAAPGLLDLALGCFPAL 180

Qy 172 RVSENNMRKLLD--ETKYPGLTLWAETFAADPAVKGLLPETELVFFAKILQKW 225  
Db 181 RACERLHGLSLIDASATATPLLDGWSQRFQAAHAPAAKRVLPDTEKVQVQTRFLQAF 236

RESULT 9  
Ti0825  
auxin-induced protein (clone MII-4) - mung bean (fragment)  
C;Species: Vigna radiata (mung bean)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 26-Aug-1999  
C;Accession: T10825  
R;Chen, J.; Wu, D.; Witham, F.H.; Heuser, C.W.; Arteca, R.N.  
submitted to the EMBL Data Library, February 1995  
A;Description: Molecular cloning and characterization of auxin-regulated genes from mung  
A;Reference number: Z17176  
A;Accession: T10825  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-230 <CHE>  
A;Cross-references: EMBL:U20809; NID:g1184122; PID:g1184123  
A;Experimental source: strain Wilcz cv. Berken; tissue\_type hypocotyl; clone MII-4  
C;Superfamily: auxin-induced protein

Query Match 34.4%; Score 411; DB 2; Length 230;  
Best Local Similarity 44.4%; Pred. No. 3.9e-26;  
Matches 92; Conservative 31; Mismatches 76; Indels 8; Gaps 4;

Qy 14 SPFALRVQIALNLKGLDYEVVEETLNPKESELLKSNPVHKKIPVFFGDKVICESALIVE 73  
Db 21 SPFFCRVKIALKLVGEYKVEYFNFRNKSEQLLYNPVHKKVPVFFVHGDKPLPSLVIVE 80

Qy 74 YIDEVWSNNALSILPQAYDRANARFWVSVIDDKWL-TSLKSVLATEDDEAKLHFEQAE 132  
Db 81 YIDETWNN--PILASDPQALARFWSKFIDDKIVGASWKSVTVDEREK-----NIA 134

Qy 133 EVLEKVEEVFNKCSGKAYFGGDYIGFVIGFSFLSFIIRVSENNMRKLLDETYPGLT 192

Db 135 ETYESLOFLNEIKE-KKFFGGBELGLVDIAAVVAFWFIQIAGLELTSEKFPNLY 193  
Qy 193 LWAEETFAADPAVKGLLPETELKLVFEAK 219  
Db 194 RWSQEFNLNHPVIXESLPPRPDPVFAFFK 220

RESULT 10  
S1636  
parC protein - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-Sep-1999  
C;Accession: S19185  
R;Takahashi, Y.; Nagata, T.  
submitted to the EMBL Data Library, February 1992  
A;Description: Differential expression of an auxin-regulated gene, parC, and a novel rel  
A;Reference number: S19182  
A;Accession: S19185  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-221 <TAK>  
A;Cross-references: EMBL:X64398; NID:g19905; PIDN:CAA45740.1; PID:g19906  
C;Superfamily: auxin-induced protein

Query Match 34.4%; Score 410.5; DB 2; Length 221;  
Best Local Similarity 41.4%; Pred. No. 4e-26;  
Matches 94; Conservative 31; Mismatches 91; Indels 11; Gaps 3;

Qy 1 MAERDLRLGAWSPFPALRVQIALNLKGLDYEVVEETLNPKESELLKSNPVHKKIPVFFH 60  
Db 1 MANEEVILLDFWPSMFGMRURIALAEKEIKYEQEDLRNKSPLLQMNPIHKKIPVLIH 60

Qy 61 GDKVICESAIIVEYIDEVWSNNALSILPQAYDRANARFWVSVIDDKWLSKSVLAT-- 118  
Db 61 NGXPICESIAVYIEEVWVKDAPSLPSPDYDRAQARFWADYIDKLYDFGRKLWATKG 120

Qy 119 EDDEAKLHFEQAEVLEKVEVFNKCSGKAYFGGDYIGFVIGFSFLSFIIRVSENNM 178  
Db 121 EQEAAKKDFIECLKVLE-----GALGDRPYFGGESFGFVDIALTGFSWFYAYETFG 173

Qy 179 ERKLLDETKYPGLTLWAETFAADPAVKGLLPETELKLVFEAKILQKW 225  
Db 174 --NFSTEAECPKFVAMAKRCMQRESVAKSLPDQPKVLEFVKVLQKF 218

RESULT 11  
S1636  
auxin-induced protein (clone pCNT107) - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Sep-1998  
C;Accession: S16636  
R;van der Zaal, E.J.; Droog, F.N.J.; Boot, C.J.M.; Hensgens, L.A.M.; Hoge, J.H.C.; Schil  
Plant Mol. Biol. 16, 983-998, 1991  
A;Title: Promoters of auxin-induced genes from tobacco can lead to auxin-inducible and r  
A;Reference number: S16267; MUID:91322513; PMID:1863770  
A;Accession: S16636  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-221 <ZAA>  
A;Cross-references: EMBL:X56266  
C;Superfamily: auxin-induced protein

Query Match 34.1%; Score 407.5; DB 2; Length 221;  
Best Local Similarity 40.3%; Pred. No. 7.1e-26;  
Matches 94; Conservative 29; Mismatches 87; Indels 23; Gaps 4;

Qy 1 MAERDLRLGAWSPFPALRVQIALNLKGLDYEVVEETLNPKESELLKSNPVHKKIPVFFH 60  
Db 1 MANEEVILLDFWPSMFGMRURIALAEKEIKYEQEDLRNKSPLLQMNPIHKKIPVLIH 60

Qy 61 GDKVICESAIIVEYIDEVWSNNALSILPQAYDRANARFWVSVIDDK-----WLTSL 112  
Db 61 NGXPICESIAVYIEEVWVKDAPSLPSPDYDRAQARFWADYIDKLYDFGRKLWTK- 119



Qy 113 KSVLATEDDEAKLHFEQAERVLKVEVPNFKSEKAYFGDGTIGFVDIGFSGFLSPFR 172  
Db 120 -----GBEQEAAXKDFIECLKVLK-----GALGDKPYFGGESFGFVDIALIGYISWFY 167  
Qy 173 VSENNERKLLDTEKYFGLTWAETFAADPAVKGLLPETEKLVFAKILQK 225  
Db 168 AYETFG--NFSTEAECPKFAVAKRCMQRESVAKSLDPQPKLVFVKLRQKF 218

RESULT 12  
T09807

probable glutathione transferase (EC 2.5.1.18) - upland cotton (fragment)  
N;Alternate names: probable glutathione S-transferase  
C;Species: Gossypium hirsutum (upland cotton)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Nov-2000  
C;Accession: T09807  
R;Yamamoto, E.; Baird, W.V.  
submitted to the EMBL Data Library, May 1998  
A;Reference number: Z16864  
A;Accession: T09807  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-161 <YAM>  
A;Cross-references: EMBL:AF064201; NID:G3135692; PID:G3135693  
A;Experimental source: fiber  
C;Genetics:  
A;Gene: GST  
C;Superfamily: auxin-induced protein  
C;Keywords: transferase

Query Match 33.7%; Score 403; DB 2; Length 161;  
Best Local Similarity 51.0%; Pred. No. 1.1e-25;  
Matches 78; Conservative 28; Mismatches 45; Indels 2; Gaps 1;  
Qy 70 IIVYIDVSWNNALSILPONAYDRANARFVWSYIDDKWLTSLKSVLATEDEAKLHFE 129  
Db 2 IIVYIDVSWP--SAPILSPDHPERATARFAAYLDDKWFPSLRAIGMAEGEDARKAIG 59  
Qy 130 QAEEVLKVEKVERVFNKSEKAYFGDGTIGFVDIGFSGFLSPFIRSENNERKLLDTEKYF 189  
Db 60 QVEGGLMLEEAFKCGQQAFFKQDQIGYLDITFGCSGLWLRVTERKSGIKLINEINTP 119

Qy 190 GLTLWAETFAADPAVKGLLPETEKLVFAKILQ 222  
Db 120 ALLKWANRNCNDAAVKQVMPETEKLABFAKMLR 152

RESULT 13  
A36225  
auxin-regulated protein, protoplast - common tobacco (cv. Xanthi nc)  
N;Alternate names: Gene str246C protein  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 17-Nov-2000  
A;Accession: A36225; S52624; A36263; A36206; JQ0631; S47431; S47443  
R;Takahashi, Y.; Kuroda, H.; Tanaka, T.; Machida, Y.; Takebe, I.; Nagata, T.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9279-9283, 1989  
A;Title: Isolation of an auxin-regulated gene cDNA expressed during the transition from  
A;Reference number: A36225; MUID:90083251; PMID:2594768  
A;Accession: A36225  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-220 <TAK>  
A;Cross-references: GB:M29274; NID:G170282; PIDN:AAA67894.1; PID:G170283  
R;Froissard, D.; Gough, C.; Czarnic, P.; Schneider, M.; Toppan, A.; Roby, D.; Marco, Y.  
Plant Mol. Biol. 26, 515-521, 1994  
A;Title: Structural organization of str 246C and str 246N, plant defense-related genes  
A;Reference number: S52623; MUID:95036027; PMID:7948901  
A;Accession: S52624  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-220 <FRO>  
A;Cross-references: EMBL:X80829; NID:G530739; PIDN:CAA56790.1; PID:G530740

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
A;Accession: S52623  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 48-194 <FRW>  
A;Cross-references: EMBL:X80828; NID:G530737; PIDN:CAA56789.1; PID:G530738  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
R;Takahashi, Y.; Niwa, Y.; Machida, Y.; Nagata, T.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8013-8016, 1990  
A;Title: Location of the cis-acting auxin-responsive region in the promoter of the par g  
A;Reference number: A36206; MUID:91045927; PMID:2236015  
A;Accession: A36206  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-106 <TA2>  
A;Cross-references: GB:D90215; NID:G218295; PIDN:BAA14243.1; PID:G218296  
C;Genetics:  
A;Gene: par  
A;Introns: 106/3  
C;Superfamily: auxin-induced protein

Query Match 33.6%; Score 402; DB 2; Length 220;  
Best Local Similarity 41.2%; Pred. No. 2e-25;  
Matches 94; Conservative 78; Mismatches 78; Indels 18; Gaps 7;  
Qy 1 MAERDLRLGAWFPPALRVQIALNLKGLDYEVVETLNPKESELLKSNPVHKKIPVFFH 60  
Db 1 MESNNVLLDFWPFSSFGMLRIALALGKIYEKENLSDKSPILLEMPNVHKKIPILIH 60  
Qy 61 GDKVICSALIVEYIDVSWNNALSILPONAYDRANARFVWSYIDDKWLTSLKSVLA-- 117  
Db 61 NSKAICESNLISYIDVW-HDKCPLLPSPYERSQARFWADYIDKIIYSTGRVWSGKG 119  
Qy 118 TEDDEAKLHFEQAEEVLEKVE-EVFNKSEKAYFGDGTIGFVDIGFSGFLSPFIRVSEN 176  
Db 120 EDQEEAKK---EFIEILKTLGELGN-----KTYFGDNLGFDVALVPTSWFYSVET 170  
Qy 177 MNERKLLDTEKYFGLTWAETFAADPAVKGLLPETEKLVFAKILQK 224  
Db 171 CANFSI--EAECPLVVMWAKTMESESVSKSLPHPHKIYGF--VLELK 214

RESULT 14

S66354  
glutathione transferase (EC 2.5.1.18), auxin-inducible - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 16-Feb-2001  
A;Accession: S66354; S71497; E84696; S57711  
R;van der Kop, D.A.M.; Schuyter, M.; Scheres, B.; van der Zaal, B.J.; Hooykaas, P.J.J.  
Plant Mol. Biol. 30, 839-844, 1996  
A;Title: Isolation and characterization of an auxin-inducible glutathione S-transferase  
A;Reference number: S66354; MUID:96194465; PMID:8624414  
A;Accession: S66354  
A;Molecule type: DNA  
A;Residues: 1-224 <VAN>  
A;Cross-references: EMBL:X89216; NID:G895699; PIDN:CAA61504.1; PID:G895700  
A;Accession: S71497  
A;Molecule type: mRNA  
A;Residues: 1-224 <VAX>  
A;Cross-references: GB:X89216; NID:G895699; PIDN:CAA61504.1; PID:G895700  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: E84696  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-224 <STO>  
A;Cross-references: GB:AE002093; NID:G3980390; PIDN:AAC95193.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At103-1a; At2g29450

A:Map position: 2  
A:introns: 106/3  
C:Superfamily: auxin-induced protein  
C:Keywords: transferase

Query Match 33.4%; Score 399; DB 2; Length 224;  
Best Local Similarity 41.1%; Pred. No. 3.5e-25;  
Matches 90; Conservative 39; Mismatches 80; Indels 10; Gaps 5;  
  
Qy 1 MAER-DLRLLGAWFSPALRVQIALNLKGLDYEVEVETLNPKSELLKSNPVHKKIPVFF 59  
Db 1 MAEEVKLLGIWASPSRRVEMALKGIPYEVVEILENKSPILLALNPIHKKVPVIV 60  
  
Qy 60 HGDKVICESAIIVYIDEVWSNNALSILPQNAYDRANARFWVSIDDKWLTSKSLVATE 119  
Db 61 HNGKTILESHVILEVIDETWPN--PILPQDPYERSKARPAKLVDQIMNVGFSIMARA 118  
  
Qy 120 DDEAKKLHFEQAEVLEKVEVFNKCEGKAYFGDDTIGFVDIGFGSFLSFI--RVSENM 177  
Db 119 DEKREVLAEQVRELIMYLE---KELVGKDYFGKTVGFLDFVAGSLIPFCLERGWEGI 174  
  
Qy 178 NERKLLDETYPGLTLWAETFAADPAVKGLLPETEKLVE 216  
Db 175 G-LEVIITEKPEPKRWNRNLEKVEIVKDCVPPREHVE 212

## RESULT 15

G84696  
Probable glutathione S-transferase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: G84696  
M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: G84696  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-225 <STO>  
A:Cross-references: GB:AE002093; NID:G3980388; PIDN:AAC95191.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g29470  
A:Map position: 2  
C:Superfamily: auxin-induced protein

Query Match 33.3%; Score 397.5; DB 2; Length 225;  
Best Local Similarity 38.9%; Pred. No. 4.7e-25;  
Matches 88; Conservative 54; Mismatches 61; Indels 23; Gaps 9;  
  
Qy 1 MAERD--LRLLGAWFSPALRVQIALNLKGLDYEVEET-LNPKSELLKSNPVHKKIPV 57  
Db 1 MAEEKGVKLTGWSWSPSPRRVEMALKGVPYDLDYLVVKSPLLLQNLNVPYKKVPV 60  
  
Qy 58 FFHGDKVICSAIIVYIDEVWSNNALSILPQNAYDRANARFWVSIDDK-WLTSLSKSLV 116  
Db 61 LVHNGKILPESQLILEYIDQWTWN--PILPQSPYDKAMARFAKFDVEQVTMIGLSLV 118  
  
Qy 117 ATEDDEAKKLHFEQAEVLEKVEVFNKCEGKAYFGDDTIGFVDIGFGSFLSFI-- 170  
Db 119 KSE-----KRIDVAIEVQELIMLENQIT-GKKLFGGETIGFLDMVVGSMIPFCL 168  
  
Qy 171 IRVSENMRKLLDETYPGLTLWAETFAADPAVKGLLPETEKLVE 216  
Db 169 ARAWEGMG-IDMIEPKFPFELNRWIKNLKEIIVRECIPDREKHIE 213

Search completed: October 8, 2004, 09:24:56  
Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2004, 09:19:41 ; Search time 32 Seconds  
(without alignments)  
374.288 Million cell updates/sec

Title: US-10-088-945A-10

Perfect score: 1195

Sequence: 1 MARDURLLGAWSPFALRV.....KLVEFAKILQKWAARAAK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
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- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000.5	83.7	234	3	US-08-924-747-8
2	1000.5	83.7	234	3	US-09-247-373B-8
3	1000.5	83.7	234	3	US-09-296-715-8
4	530.5	44.4	236	3	US-09-248-335-74
5	512.5	42.9	232	3	US-09-248-335-56
6	511	42.8	227	3	US-09-248-335-48
7	504	42.2	225	3	US-09-248-335-62
8	501	41.9	236	3	US-09-248-335-68
9	489	40.9	228	3	US-09-248-335-70
10	484.5	40.5	240	3	US-09-248-335-42
11	481	40.3	231	3	US-09-248-335-54
12	466	39.0	225	3	US-08-924-747-14
13	466	39.0	225	3	US-09-247-373B-14
14	466	39.0	225	3	US-09-296-715-14
15	459.5	38.5	233	3	US-09-248-335-60
16	458	38.3	225	3	US-09-248-335-40
17	450.5	37.7	225	3	US-08-924-747-10
18	450.5	37.7	225	3	US-09-247-373B-10
19	450.5	37.7	225	3	US-09-296-715-10
20	450	37.7	221	3	US-09-247-373B-54
21	446	37.3	224	3	US-09-247-373B-34
22	444	37.2	225	3	US-08-924-747-16
23	444	37.2	225	3	US-09-247-373B-16
24	444	37.2	225	3	US-09-296-715-16
25	433.5	36.3	203	3	US-09-248-335-58
26	428.5	35.9	229	3	US-09-247-373B-48
27	428.5	35.9	235	3	US-09-248-335-64

Sequence 46, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 52, Appl  
Sequence 66, Appl  
Sequence 38, Appl  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 6, Appl  
Sequence 20, Appl

28 421.5 35.3 227 3 US-09-248-335-46  
29 410.5 34.4 220 3 US-08-924-747-26  
30 410.5 34.4 220 3 US-09-247-373B-26  
31 410.5 34.4 220 3 US-09-296-715-26  
32 409.5 34.3 219 3 US-09-247-373B-52  
33 408 34.2 222 3 US-09-248-335-66  
34 408 34.1 238 3 US-09-248-335-38  
35 404.5 33.8 222 3 US-08-924-747-22  
36 404.5 33.8 222 3 US-09-247-373B-22  
37 404.5 33.8 222 3 US-09-296-715-22  
38 404 33.8 200 3 US-09-248-335-72  
39 402 33.6 200 3 US-08-924-747-18  
40 402 33.6 200 3 US-09-247-373B-18  
41 402 33.6 200 3 US-09-296-715-18  
42 399.5 33.4 225 3 US-09-247-373B-36  
43 398 33.3 220 3 US-09-247-373B-50  
44 393 32.9 219 3 US-08-924-747-6  
45 393 32.9 219 3 US-08-924-747-20

#### ALIGNMENTS

#### RESULT 1

US-08-924-747-8  
; Sequence 8, Application US/08924747  
; Patent No. 6063570  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE  
; TITLE OF INVENTION: ENZYMES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
; SOFTWARE: MICROSOFT WORD VERSION 7.0A  
; CURRENT APPLICATION NUMBER: US/08/924,747  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: CL-1108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: SOYBEAN  
; IMMEDIATE SOURCE:  
; CLONE: SEQ.03B09  
; US-08-924-747-8

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
Best Local Similarity 84.6%; Pred. No. 1.8e-98;  
Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
Db 6 DLKLLGGWFSFALRVQIALNLKGLDYEVVEETLNPKSDLLKSNPVHKKIPVFFHGDV 65  
  
Qy 65 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
Db 66 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
  
Qy 125 KLHFEQAEEVLEKVEEVFNKSEKAYFGGDTIGFVDIGFSGFSLFIRVSNMNERKLLD 184  
Db 125 KPHEQAEEGLERLEEVFNKSEKAYFGGDSIGFIDIGFSGFSLVVAEDDEAK 184  
  
Qy 185 ETKYPGLTMAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAAA 231  
Db 185 EKKHPGLTQWAEETFAADPAVKGLLPETDKLVFEPAKILQLKWTATAAAA 231

## RESULT 2

US-09-247-373B-8  
; Sequence 8, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; CURRENT FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 08/924,747  
; PRIOR FILING DATE: 1997-09-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 8  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: SOYBEAN  
US-09-247-373B-8

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
Best Local Similarity 84.6%; Pred. No. 1.8e-98;  
Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;  
  
Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
Db 6 DLKLLGGWFSFALRVQIALNLKGLDYEVVEETLNPKSDLLKSNPVHKKIPVFFHGDV 65  
  
Qy 65 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
Db 66 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
  
Qy 125 KLHFEQAEEVLEKVEEVFNKSEKAYFGGDTIGFVDIGFSGFSLFIRVSNMNERKLLD 184  
Db 125 KPHEQAEEGLERLEEVFNKSEKAYFGGDSIGFIDIGFSGFSLVVAEDDEAK 184  
  
Qy 185 ETKYPGLTMAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAAA 231  
Db 185 EKKHPGLTQWAEETFAADPAVKGLLPETDKLVFEPAKILQLKWTATAAAA 231

## RESULT 3

US-09-296-715-8  
; Sequence 8, Application US/09296715  
; Patent No. 6171839  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE  
; TITLE OF INVENTION: ENZYMES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON

; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
; SOFTWARE: MICROSOFT WORD VERSION 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/296,715  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: CL-1108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; TISSUE TYPE: SOYBEAN  
; IMMEDIATE SOURCE:  
; CLONE: SE3.03B09  
US-09-296-715-8

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
Best Local Similarity 84.6%; Pred. No. 1.8e-98;  
Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;  
  
Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
Db 6 DLKLLGGWFSFALRVQIALNLKGLDYEVVEETLNPKSDLLKSNPVHKKIPVFFHGDV 65  
  
Qy 65 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
Db 66 ICESAIIVEYIDEVSNALSIIPQAYDRANARFWYSYIDDKWLTSKSLVATEDDEAK 124  
  
Qy 125 KLHFEQAEEVLEKVEEVFNKSEKAYFGGDTIGFVDIGFSGFSLFIRVSNMNERKLLD 184  
Db 125 KPHEQAEEGLERLEEVFNKSEKAYFGGDSIGFIDIGFSGFSLVVAEDDEAK 184  
  
Qy 185 ETKYPGLTMAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAAA 231  
Db 185 EKKHPGLTQWAEETFAADPAVKGLLPETDKLVFEPAKILQLKWTATAAAA 231

## RESULT 4

US-09-248-335-74  
; Sequence 74, Application US/09248335  
; Patent No. 6096504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 08/924,759  
; EARLIER FILING DATE: 1997-September-05  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 74  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: maize  
US-09-248-335-74

```
Query Match 44.4%; Score 530.5; DB 3; Length 236;
Best Local Similarity 47.2%; Pred. No. 2.1e-46;
Matches 109; Conservative 48; Mismatches 65; Indels 9; Gaps 4;

QY 5 DLRLGAWFPPFALRVQIALNLKGLDYEVVEETIN-PKSELLKSNPVHKKIPVFFHGDK 63
DB 8 ELKLGAWASPPFVLRVKLALSFGLSYEDVEDLSGCKSELLLESNPVHKKVPVLLHNGK 67

QY 64 VICESAIIVYIDEVWNNALSILPQDAYDRANARFWVSYYDDK---WLTSLKSVLATE 119
DB 68 PVCESQIIIVQYIDEAFAGTGPSLLPADPHQRAVARFAGYIDDKLLAFWLQSARA--KTQ 125

QY 120 DDEAKKLHFEQAEVLEKVEEVNKCSEKAYFGGDTIGFVDFGSGFLSFIRVSENME 179
DB 126 EEKAEAL--KOALAAEENLEAFTETSEKPFPGGDSVGYLDVTLGALVAVHAAEKLGY 183

QY 180 RKLLDETKYPGTLTWAETFAADPAVKGLLPETEKLVFAKILQKWAASAAA 230
DB 184 MRLFDATRTPLSNFVERFGALGNAAKAVLPDVDGLVEYAKORQADAAAAS 234

RESULT 5
US-09-248-335-56
; Sequence 56, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 56
; LENGTH: 232
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-56

Query Match 42.9%; Score 512.5; DB 3; Length 232;
Best Local Similarity 46.3%; Pred. No. 1.7e-46;
Matches 101; Conservative 41; Mismatches 75; Indels 1; Gaps 1;

QY 1 MAERDLRLGAWFPPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
DB 1 MSEAARVIGLWSPFVIRVLIALLKLGVEFEFVEEVVGRKSELLLSRNPVHKKIPVLLH 60

QY 61 GDKVICSALIVYIDEVWNNALSILPQDAYDRANARFWVSYYDDKWLTSKSVLATE 120
DB 61 HGKPLSESLIIVQYIDEVWSSGAPAFIPVDAHARAVQRFWAQYVDDKLPWAIR-ILKGTD 119

QY 121 DEAKKLHFEQAEVLEKVEEVNKCSEKAYFGGDTIGFVDFGSGFLSFIRVSENME 180
DB 120 DGGMEQAGQLSAALLQLEEAFAQLSQGRYFGGDSVGYLDIALVSHGVVKAVEKIAGV 179

QY 181 KLADETKYPGLTWAETFAADPAVKGLLPETEKLVFA 218
DB 180 TLLDKAKVPLNVAWADRLCAHPAVVDAIPDADKFEVS 217

RESULT 6
US-09-248-335-48
; Sequence 48, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
```

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; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 48
; LENGTH: 237
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-48

Query Match 42.8%; Score 511; DB 3; Length 237;
Best Local Similarity 44.7%; Pred. No. 2.5e-46;
Matches 101; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 6 LRLGAWFPPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDKVI 65
DB 11 LKLGAWSPFVNRVRMALHLKGLYEVENVEDLTNKSDDLILASNPVHKLVPVLLHGDKPI 70

QY 66 CESAIIVYIDEVWNNALSILPQDAYDRANARFWVSYYDDKWLTSKSVLATEDEDAKK 125
DB 71 SESLIVIVEYLDLDDAFPGAGQAVLPADPYERAVARFWAKYVDGKLUHGMVVKALMGATEERA 130

QY 126 LHFEQAEVLEKVEEVNKCSEKAYFGGDTIGFVDFGSGFLSFIRVSENMEERKLLDE 185
DB 131 TATVDALAAMDITLEGAFACSGGKFPAGDAPGYLDVALGGFICGLRAWDKVGVKLLDA 190

QY 186 TKYPGLTWAETFAADPAVKGLLPETEKLVFAKILQKWAASAAA 231
DB 191 GRVPRLATWAERFAALDVAKEVIPDPDTHIAEFAKVLQARSAAATS 236

RESULT 7
US-09-248-335-62
; Sequence 62, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 62
; LENGTH: 225
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-62

Query Match 42.2%; Score 504; DB 3; Length 225;
Best Local Similarity 46.6%; Pred. No. 1.3e-45;
Matches 102; Conservative 38; Mismatches 77; Indels 2; Gaps 2;

QY 1 MAERDLRLGAWFPPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60
DB 1 MSEAARVIGLWSPFVIRVLIALLKLGVEFEFVEEVVGRKSELLLSRNPVHKKIPVLLH 60

QY 61 GDKVICSALIVYIDEVWNNALSILPQDAYDRANARFWVSYYDDKWLTSKSVLATE 119
DB 61 HGKPLSESLIIVQYIDEVWSSGAPAFIPADPYARAVQRFWAQYVDDKMPHPAIRVLKGTY 120

QY 120 DDEAKKLHFEQAEVLEKVEEVNKCSEKAYFGGDTIGFVDFGSGFLSFIRVSENME 179
DB 121 DGD-KEQAAGQLSAAQLLEEAFAQLGQGRYFGGDSVGYLDIALVSHGVVKAVEKIAG 179

QY 180 RKLLDETKYPGLTWAETFAADPAVKGLLPETEKLVFA 218
DB 180 VTLLDEAKVPLNVAWADRLCAHPAVVDAIPDADKFEVS 218
```

```
RESULT 8
US-09-248-335-68
; Sequence 68, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 68
; LENGTH: 236
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-68

Query Match 41.9%; Score 501; DB 3; Length 236;
Best Local Similarity 45.5%; Pred. No. 2.8e-45;
Matches 102; Conservative 39; Mismatches 79; Indels 4; Gaps 2;

Qy 1 MAERD--LRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVF 58
Db 5 VADKDPKLVGVWSSPFVIRARVALNLKGLAYRYVEDNLDKSELLASNPHVHGKVPVL 64

Qy 59 FHGDKVICSIAIIVEYDEVWNNALSILPONAYDRANARFWVSYYIDDKLTSLKSVLAT 118
Db 65 LHDGRPVCSRVIVEYIDEAPPASGCLLPADPYRRADVRFWASYADDKLFPPTWIPYNG 124

Qy 119 EDDAKKLHFEQAEVLEKVEEVNKC--SEKAYFGDDTIGFVDIGFGSFLSFIRVSEN 176
Db 125 RTSDDRVAARQVAVVLEKFEQAEDECSGGKGAFFGGDAAGLVDDVVGLGFLGWLRASEA 184

Qy 177 MNERKLIDETKYPGLTLWAETFAADPAVKGLLPETEKLVFPAKI 220
Db 185 MCGVRVIDPAKTPLLAAWADRFAALDGVREIVDPVQRLLLEYNKI 228

RESULT 9
US-09-248-335-70
; Sequence 70, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 70
; LENGTH: 228
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-70

Query Match 40.9%; Score 489; DB 3; Length 228;
Best Local Similarity 47.4%; Pred. No. 5.1e-44;
Matches 102; Conservative 31; Mismatches 80; Indels 2; Gaps 2;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFHGDV 64
Db 8 ELKLLGVWDSFYVNRVQIVLNLKGLSYEVEDLDSKSELLNLSNPVHKKVPVLIHAGKP 67
```

```
Qy 65 ICESAIIVEYDEVWNNAL-SILPONAYDRANARFWVSYYIDDKLTSLKSVLATDEDEA 123
Db 68 VAESQAIQVLDFAFPSTGTPPSVLPAPPYARATARFAAFVDDKVGSPMHTVLFARSHGK 127

Qy 124 KKLHFEQAEVLEKVEEVNKCSEKAYFGDDTIGFVDIGFGSFLSFIRVSENNERKLL 183
Db 128 KADAASRIVAALLETLEGAFCDCSGGRDYFGDDAIGFVDVVLGSLYLGHWFKVFERKMGVRVL 187

Qy 184 DETKYPGLTLWAETFAADPAVKGLLP-ETEKLVF 217
Db 188 DVARTPLLAANGERFAAAEAADKVLDDVDKVLFF 222

RESULT 10
US-09-248-335-42
; Sequence 42, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 42
; LENGTH: 240
; TYPE: PRT
; ORGANISM: maize
US-09-248-335-42

Query Match 40.5%; Score 484.5; DB 3; Length 240;
Best Local Similarity 44.0%; Pred. No. 1.7e-43;
Matches 102; Conservative 39; Mismatches 78; Indels 13; Gaps 4;

Qy 6 LRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFPHGDKVI 65
Db 11 LTLGLHVSFPALRVRMALSLKGLSYEYIBQDLPHKGELLSSNPVHKKVPVLIHHGKPI 70

Qy 66 CESAIIVEYDEVWNNALSILPONAYDRANARFWVSYYIDDK----WLTSLKSVLATDEDD 121
Db 71 CESLAVVEYDEVWPGAAATILPADPHGRATARFWAAYIDGKLFPAPWTGIMKA--ATEEA 128

Qy 122 EAKKLHFEQAEVLEKVEEVNKC-----EGKAYFGDDTIGFVDIGFGSFLSFIRVSEN 176
Db 129 RADKL--RETHAAVLNLEKAFABEISSSSSNDGAFFGGDSVGVYLDLALGCSLPWFGLRA 186

Qy 177 MNERKLIDETKYPGLTLWAETFAADPAVKGLLPETEKLVFPAKILQLKWA 228
Db 187 MLGVEIIDAQAQAPLLVAAERFGETPVAKEVLPQDPAVAYAKKIQAYWASA 238

RESULT 11
US-09-248-335-54
; Sequence 54, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 54
; LENGTH: 231
; TYPE: PRT
```



CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER:.. US/09/296,715  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: FLOYD, LINDA AXAMETHY  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: CL-1108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-892-8112  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
TISSUE TYPE: SOYBEAN  
CLONE: SES8W.PK0028.C6  
US-09-296-715-14

Query Match 39.0%; Score 466; DB 3; Length 225;  
Best Local Similarity 45.9%; Pred. No. 1.4e-41;  
Matches 100; Conservative 37; Mismatches 73; Indels 8; Gaps 4;

Qy 3 ERDLRLIGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPNVHKKI PVFFHGD 62  
Db 5 QEDVKLLGATGSPFVCRVQIALKLGQVYKFEENLNKSELLKSNPNVHKKI PVFFHNE 64  
Qy 63 KVICESAIIVEYIDEVMSNNALSILPONAYDRANARFWVSYYDDKWLTSLSKSVLATEDE 122  
Db 65 KPIAESLIVIVEYIDETWKN--PILPSDPYQALAREFWSKFIIDKVVGAAMWKYITVDEK 122  
Qy 123 AKLHFQAEVLEKVEEVFNKCEGKAYFGDITIGFVDSFLSFIRVSENMMERK 181  
Db 123 EREKNVEESYBALQFLENEL----KDKKFGGEEIGLVLDIA-AVFIAPWIPIIQEVILGLK 177  
Qy 182 LLDETKYPGLTLWAETFAADPAVKGLLPETEKLVEFAK 219  
Db 178 LFTSEKPKLYKMSQEFINHPVKVQLPPRDQLFAFYK 215

RESULT 15  
US-09-248-335-60  
Sequence 60, Application US/09248335  
Patent No. 6096504  
GENERAL INFORMATION:  
APPLICANT: MCGONIGLE, BRIAN  
APPLICANT: O'KEEF, DANIEL  
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
FILE REFERENCE: CL-1128-A  
CURRENT APPLICATION NUMBER: US/09/248,335  
CURRENT FILING DATE: 1999-02-10  
EARLIER APPLICATION NUMBER: 08/924,759  
EARLIER FILING DATE: 1997-September-05  
NUMBER OF SEQ ID NOS: 74  
SOFTWARE: Microsoft Word Version 7.0A  
SEQ ID NO 60  
LENGTH: 233  
TYPE: PRT  
ORGANISM: maize

US-09-248-335-60

Query Match 38.5%; Score 459.5; DB 3; Length 233;  
Best Local Similarity 43.6%; Pred. No. 7.3e-41;  
Matches 99; Conservative 40; Mismatches 83; Indels 5; Gaps 3;  
Qy 6 LRLIGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPNVHKKI PVFFHGDKVI 65  
Db 7 LKVLGLQVSPFVLRVCMALNTKGVSYEVEEDLSNKSSELLKSNPNVHKKVPLIHNGKPI 66  
Qy 66 CESAIIVEYIDEVMSNNALSILPONAYDRANARFWVSYYDDKWLTSLSKSVLATEDEAKK 125  
Db 67 CESLVIMQYVDELFAGR--SILPTDPYERATARFWAAYADDKLLPAWYGMVKAQSABERA 124  
Qy 126 LHFEQAEVLEKVEEVFNKCEGK-AVFGDITIGFVDSFLSFIRVSENMMERKLLD 184  
Db 125 EKVEETLSAIQHMEVAFKCGGNAAFPGDSIGYVDIVLGSFLFWFEAVRRVYDLEIN 184  
Qy 185 ETKYPGTLTLWAETFAADPAVKGLLPETEKLVEFAKILQLKWAASAAAA 231  
Db 185 ASNTPLLLAAWAERFVGTVEAKEVVPVPD--VDMAVQCINKLHAPAAA 229

Search completed: October 8, 2004, 09:25:33  
Job time : 33 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2004, 09:04:30 ; Search time 123 Seconds  
(without alignments)  
532.935 Million cell updates/sec

Title: US-10-088-945A-10  
Perfect score: 1195  
Sequence: 1 MAERDLRLGAWFSPALRV.....KLVEFAKILQKWAAAAAK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	232	4	AAB62226 Glycine m
2	1000.5	83.7	234	3	AAB03734 Clone se3
3	1000.5	83.7	234	3	AAY79515 Soybean g
4	1000.5	83.7	234	3	AAB07829 Amino aci
5	1000.5	83.7	234	4	AAB66733 Soybean t
6	1000.5	83.7	234	4	AAB62227 Glycine m
7	638	53.4	227	5	ABB90937 Herbicida
8	624	52.2	233	4	AAB47340 GST3. 9/2
9	623	52.1	233	4	AAB47339 GST2. 9/2
10	607	50.8	233	4	AAB47341 GST conse
11	596	49.9	234	5	ABB91390 Herbicida
12	585.5	49.0	234	3	AAG26676 Arabidops
13	585.5	49.0	281	3	AAG26675 Arabidops
14	585.5	49.0	287	3	AAG26674 Arabidops
15	558	46.7	233	3	AAG53029 Arabidops
16	558	46.7	233	5	ABB91389 Herbicida
17	558	46.7	241	3	AAG53028 Arabidops
18	554	46.4	233	3	AG111459 Arabidops
19	554	46.4	241	3	AG111458 Arabidops
20	530.5	44.4	236	3	AAB22136 Maize glu
21	526	44.0	227	3	AAG08276 Arabidops
22	526	44.0	245	3	AAG08275 Arabidops
23	523.5	43.8	233	2	AAY05544 Wheat Typ
24	520	43.5	227	3	AG431149 Arabidops
25	520	43.5	227	5	ABB91146 Herbicida

26	512.5	42.9	232	3	AAB22127	Aab22127 Maize glu
27	511	42.8	237	3	AAB22123	Aab22123 Maize glu
28	504	42.2	225	3	AAB22130	Aab22130 Maize glu
29	501	41.9	236	3	AAB22133	Aab22133 Maize glu
30	491.5	41.1	234	5	ABB91525	Abb91525 Herbicida
31	489	40.9	228	3	AAB22134	Aab22134 Maize glu
32	486.5	40.7	229	5	ABB91524	Abb91524 Herbicida
33	484.5	40.5	240	3	AAB22120	Aab22120 Maize glu
34	481	40.3	231	3	AAB22126	Aab22126 Maize glu
35	479.5	40.1	243	5	ABB91147	Abb91147 Herbicida
36	466	39.0	225	3	AAB03737	Aab03737 Clone ses
37	466	39.0	225	3	AAY79518	Aay79518 Soybean g
38	466	39.0	225	3	AAB07832	Aab07832 Amino aci
39	466	39.0	225	4	AAB66736	Aab66736 Soybean t
40	465	38.9	170	5	ABB90938	Abb90938 Herbicida
41	459.5	38.5	233	3	AAB22129	Aab22129 Maize glu
42	458	38.3	225	3	AAB22119	Aab22119 Maize glu
43	450.5	37.7	225	3	AAB03735	Aab03735 Clone ses
44	450.5	37.7	225	3	AAY79516	Aay79516 Soybean g
45	450.5	37.7	225	3	AAB07830	Aab07830 Amino aci

## ALIGNMENTS

## RESULT 1

AAB62226  
ID AAB62226 standard; protein; 232 AA.

XX AAB62226;

XX AC

XX 11-JUN-2001 (first entry)

XX Glycine max glutathione-S-transferase (GST) 3.3.

XX Soybean; glutathione-S-transferase; GST; homogluthathione synthetase; HGS;

XX beta-alanine; gamma-glutamylcysteine; herbicide.

XX Glycine max.

XX WO200121770-A2.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-GH003573.

XX 21-SEP-1999; 99GB-00022346.

XX (ZENE ) ZENECA LTD.

XX Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I;

XX Skipsey M;

XX WPI; 2001-257978/26.

XX N-PSDB; AAF57513.

XX Novel glutathione-S-transferase and homogluthathione synthetase sequences

XX from soybean for producing plants which are resistant and tolerant to

XX herbicide comprising fomesafen and/or acifluorfen.

XX Claim 1; Page 44-45; 64pp; English.

XX The invention relates to new soybean glutathione-S-transferase (GST) and

XX a homogluthathione synthetase (HGS). The HGS is capable of catalyzing the

XX addition of beta-alanine onto gamma-glutamylcysteine. Polynucleotides

XX encoding the proteins of the invention are useful for producing plants

XX which are resistant and/or tolerant to a herbicide comprising fomesafen

XX and/or acifluorfen. Methods of the invention are useful for providing

XX plants with further desired agronomic trait, especially resistant to a

XX herbicide, comprising glyphosate or its salt. Further desired agronomic

XX traits include insect resistance, nematode resistance, stress tolerance,

XX altered field, altered nutritional value, altered quality or any other

XX desirable agronomic trait. GST or its variant is also useful as a

CC selectable marker gene. The present sequence represents a Glycine max GST  
 CC 3.3 protein (also referred to as GST 3.6)  
 XX  
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1195; DB 4; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-118; Mismatches 0; Gaps 0;  
 Matches 232; Conservative 0; Indels 0;

Qy 1 MAERDLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60  
 Db 1 MAERDLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFH 60

Qy 61 GDKVICSAIIVEYIDEVWSNNALSILPONAYDRANARFWVSYIDDKWLTSLKSVLATED 120  
 Db 61 GDKVICSAIIVEYIDEVWSNNALSILPONAYDRANARFWVSYIDDKWLTSLKSVLATED 120

Qy 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFGSFLSIRVSENNMR 180  
 Db 121 DEAKKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFGSFLSIRVSENNMR 180

Qy 181 KLLDETKYPGLTWAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAAK 232  
 Db 181 KLLDETKYPGLTWAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAAK 232

RESULT 2  
 AAB03734  
 ID AAB03734 standard; protein; 234 AA.  
 XX  
 AC AAB03734;  
 XX  
 DT 04-OCT-2000 (first entry)  
 XX  
 DE Clone se3.03b09 type III GST protein sequence.  
 XX  
 KW Soybean; glutathione-S-transferase; GST; detoxify; herbicide; stress;  
 KW transgenic plant; tolerant; plant breeding.  
 XX  
 OS Glycine max.  
 XX  
 FN US6063570-A.  
 XX  
 PD 16-MAY-2000.  
 XX  
 PF 05-SEP-1997; 97US-00924747.  
 XX  
 PR 05-SEP-1997; 97US-00924747.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Megonigle B, O'keefe DP;  
 XX  
 DR WPI; 2000-375487/32.  
 DR N-PSDB; AAA53398.  
 XX  
 XX New Glutathione-S-Transferase enzymes and isolated nucleic acid fragments  
 PT encoding them, useful for detoxifying xenobiotic compounds in plants and  
 PT seeds, as well as in producing transgenic plants that are herbicide-  
 PT resistant.  
 XX  
 PS Claim 1; Col 35-36; 36pp; English.  
 XX  
 CC This sequence represents a Glutathione-S-Transferase (GST) protein  
 CC isolated from a soybean clone. The invention relates to isolated nucleic  
 CC acid fragments (see AAA53393-A53406) which encode soybean GST  
 CC polypeptides (AAB03731-B03744). GSTs are a family of enzymes which  
 CC catalyze the conjugation of glutathione, homogluthathione and other  
 CC glutathione-like analogues, to a large range of hydrophobic,  
 CC electrophilic compounds. GSTs have been implicated in the detoxification  
 CC of certain herbicides. The GST nucleotide sequences are useful in the  
 CC construction of herbicide-tolerant transgenic plants, plants that are  
 CC tolerant to a wide variety of stresses, or plants in which the GST

CC enzymes are present at higher or lower levels than they are normally. The  
 CC nucleic acid fragments are also useful as probes for genetically and  
 CC physically mapping the genes that they are part of, and as markers for  
 CC traits linked to expression of the enzymes. This will be useful in plant  
 CC breeding in order to develop lines with desired phenotypes or in the  
 CC identification of mutants. The soybean GST enzymes are used to detoxify  
 CC xenobiotic compounds in plants and seeds. The enzymes are also useful as  
 CC targets to facilitate design and/or identify inhibitors of the enzymes  
 CC that may be used as herbicides or herbicide synergists. The GST enzymes  
 CC produced in the host cells, particularly in microbial host cells, are  
 CC useful in preparing antibodies to the enzymes. These antibodies are  
 CC useful for detecting the enzymes in situ in cells or in vitro in cell  
 CC extracts  
 XX  
 SQ Sequence 234 AA;

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-97;  
 Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
 Db 6 DLKLGWGFSPFALRVQIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 65

Qy 65 ICESAIIVEYIDEVWSNNALSILPONAYDRANARFWVSYIDDKWLTSLKSVLATEDDEAK 124  
 Db 66 ICESAIIVEYIDEAWT-NVPSILPONAYDRANARFWVSYIDDKWLTSLKSVLVAEDDEAK 124

Qy 125 KLFHFEQAEVLEKVEEVFNKCSGKAYFGGDTTIGFVDIGFGSFLSIRVSENNMRKLLD 184  
 Db 125 KPHFEQAEGLERLEEVFNKYSKGKAYFGGDSIGFIDIGFGSFLSWRVIEEMSGRKLDD 184

Qy 185 ETYPKGLTWAETFAADPAVKGLLPETEKLVFEPAKILQLKWAATAAA 231  
 Db 185 EKKHGLTQWAEETFAADPAVKGLLPETDKLVFEPAKILQLKWAATAAA 231

RESULT 3  
 AAY79515  
 ID AAY79515 standard; protein; 234 AA.  
 XX  
 AC AAY79515;  
 XX  
 DT 01-AUG-2000 (first entry)  
 XX  
 DE Soybean glutathione-S-transferase se3.03B09.  
 XX  
 KW Soybean; glutathione-S-transferase; GST; xenobiotic; detoxification;  
 KW transgenic plant; herbicide tolerance.  
 XX  
 OS Glycine max.  
 XX  
 FN WO200018936-A1.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 30-SEP-1998; 98WO-US020501.  
 XX  
 PR 30-SEP-1998; 98WO-US020501.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Megonigle B, O'keefe DP;  
 XX  
 DR WPI; 2000-317517/27.  
 DR N-PSDB; AAZ94952.  
 XX  
 PT Nucleic acids encoding soybean glutathione-S-transferase enzymes useful  
 PT for conferring herbicide resistance to plants.  
 XX  
 PS Claim 4; Page 46; 76pp; English.  
 XX  
 CC The present sequence is that a soybean class III glutathione-S-

CC transferase (GST), as deduced from soybean embryo cDNA clone se3.03B09  
 CC (see AA294952). The invention provides soybean GST enzymes (see AA79512-  
 CC 25) involved in the detoxification of xenobiotic compounds, especially  
 CC herbicides, in plants and seeds. Chimeric genes encoding all or a portion  
 CC of soybean GST, host cells, and methods of recombinant production of  
 CC soybean GST enzymes are provided. The sequences are useful in the  
 CC construction of herbicide-tolerant transgenic plants, in the recombinant  
 CC production of GST enzymes, in the development of screening assays to  
 CC identify compounds inhibitory to the GST enzymes (useful as herbicides or  
 CC herbicide synergists), and in screening assays to identify chemical  
 CC substrates of the GSTs

XX Sequence 234 AA;

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-97;  
 Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;  
 Qy 5 DLRLGAWFSPALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDKV 64  
 Db 6 DLKLLGGWFSFALRVOIALNLKGLDYEVVEETLNPKSDLLKSNPVHKKIPVFFHGDKV 65  
 Qy 65 ICESAIIIVEYIDVWSNNALSILPONAYDRANARFWYSYIDDKWLTSLKSVLATEDEAK 124  
 Db 66 ICESAIIIVEYIDEAWT-NVPSILPONAYDRANARFWAYIDEKWTSLRSVLVAEDDEAK 124  
 Qy 125 KLHPEQAEVLEKVEEVFNKCEGKAYFGGDTIGFVDIGFGSFLSFRVSNMNERKLLD 184  
 Db 125 KPHEQAEGLERLEEVFNKSEKAYFGGDSIGFIDIGFGSFLSMRVIEEMSGRKLDD 184  
 Qy 185 ETKYPGLTLWAETFAADPAVKGLLPETEKLVFPAKILQLKWAASAAA 231  
 Db 185 EKKHGLTQWAEETFAADPAVKGLLPETDKLVFPAKILQLKWTAAAAA 231

RESULT 4  
 AAB07829  
 ID AAB07829 standard; protein; 234 AA.  
 XX AC AAB07829;  
 XX DT 14-NOV-2000 (first entry)  
 XX Amino acid sequence of a soybean type III glutathione-S-transferase.  
 XX Soybean; glutathione-S-transferase; GST; detoxification;  
 XX xenobiotic compound; herbicide-tolerance; transgenic plant;  
 XX herbicide synergist.

XX Glycine max.  
 XX WO200047728-A2.  
 XX 17-AUG-2000.  
 XX 10-FEB-2000; 2000WO-US003347.  
 XX 10-FEB-1999; 99US-00247373.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Mcgonigle B, O'keefe DP;  
 XX WPI; 2000-549144/50.  
 XX N-PSDB; AAA59460.

XX Soybean glutathione-S-transferase polypeptides and polynucleotides used  
 XX to produce herbicide tolerant transgenic plants and to screen for  
 XX inhibitors or substrates of the enzyme.  
 XX Claim 4; Page 58-59; 84pp; English.

XX The present sequence represents a soybean glutathione-S-transferase (GST)

CC enzyme. The enzyme is involved in the detoxification of xenobiotic  
 CC compounds in plants and seeds. The GST polynucleotides and polypeptides  
 CC are used for the production of herbicide-tolerant transgenic plants, and  
 CC for the development of screening assays to identify GST inhibitors and  
 CC substrates, which can be used as herbicide synergists. GST Gene specific  
 CC probes can be used in gene identification methods. The recombinant GST  
 CC enzymes can be used to produce enzyme specific antibodies which are used  
 CC to detect the enzymes in situ in cells or in vitro in cell extracts

XX Sequence 234 AA;

Query Match 83.7%; Score 1000.5; DB 3; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-97;  
 Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;  
 Qy 5 DLRLGAWFSPALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDKV 64  
 Db 6 DLKLLGGWFSFALRVOIALNLKGLDYEVVEETLNPKSDLLKSNPVHKKIPVFFHGDKV 65  
 Qy 65 ICESAIIIVEYIDVWSNNALSILPONAYDRANARFWYSYIDDKWLTSLKSVLATEDEAK 124  
 Db 66 ICESAIIIVEYIDEAWT-NVPSILPONAYDRANARFWAYIDEKWTSLRSVLVAEDDEAK 124  
 Qy 125 KLHPEQAEVLEKVEEVFNKCEGKAYFGGDTIGFVDIGFGSFLSFRVSNMNERKLLD 184  
 Db 125 KPHEQAEGLERLEEVFNKSEKAYFGGDSIGFIDIGFGSFLSMRVIEEMSGRKLDD 184  
 Qy 185 ETKYPGLTLWAETFAADPAVKGLLPETEKLVFPAKILQLKWAASAAA 231  
 Db 185 EKKHGLTQWAEETFAADPAVKGLLPETDKLVFPAKILQLKWTAAAAA 231

RESULT 5  
 AAB66733  
 ID AAB66733 standard; protein; 234 AA.  
 XX AC AAB66733;  
 XX DT 09-APR-2001 (first entry)  
 XX Soybean type III GST protein #2.  
 XX Soybean; glutathione-S-transferase; herbicide; GST.

XX Glycine max.  
 XX US6171839-B1.  
 XX 09-JAN-2001.  
 XX 22-APR-1999; 99US-00296715.  
 XX 05-SEP-1997; 97US-00924747.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Mcgonigle B, O'keefe DP;  
 XX WPI; 2001-136874/14.

XX Novel soybean glutathione-S-transferase enzymes useful as targets to  
 XX facilitate design and/or identification of inhibitors of the enzyme, that  
 XX are used as herbicides or herbicide synergists.

XX Claim 1; Col 35-38; 37pp; English.

XX The present invention relates to soybean glutathione-S-transferase  
 XX proteins. The novel sequences are useful in the construction of herbicide  
 XX tolerant transgenic plants, in the recombinant production of glutathione-  
 XX S-transferase (GST) enzymes, in the development of screening assays to  
 XX identify compounds inhibitory to the GST enzymes, and in screening assays  
 XX to identify chemical substrates of the GSTs

SQ Sequence 234 AA;

Query Match 83.7%; Score 1000.5; DB 4; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-97;  
 Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVETLNPKSELLKSNPVHKKIPVFFHGDV 64  
 Db 6 DLKLLGWFSPFALRVQIALNLKGLDYEVVETLNPKSDLLKSNPVHKKIPVFFHGDV 65

Qy 65 ICESAIIIVEYIDEVMSNNALSIIPQAYDRANARFWYSYIDDKWLTSLKSVLATEDDEAK 124  
 Db 66 ICESAIIIVEYIDEAWT-NVPSILPQAYDRANARFWAYIDEKWFTSLRSVLVAEDDEAK 124

Qy 125 KLHFEQAEVLEKVEEVFNKSEKAYFGGDTIGFVDFGSGFLSFIRVSENMMERKLLD 184  
 Db 125 KPHEQAEGLERLEEVFNKSEKAYFGGDSIGFIDIGFSGFLSWRVIEEMSGRKLLD 184

Qy 185 ETKYPGLTLWAETFAADPAVKGILPETEKLVEFAKILQLKWAATAAA 231  
 Db 185 EKKHPGLTQWAEETFAADPAVKGILPETDKLVEFAKILQLKWTATAAA 231

RESULT 6  
 AAB62227  
 ID AAB62227 standard; protein; 234 AA.  
 AC AAB62227;  
 DT 11-JUN-2001 (first entry)  
 DE Glycine max clone SE3.03B09 sequence.  
 KW Soybean; glutathione-S-transferase; GST; homoglutathione synthetase; HGS;  
 KW beta-alanine; gamma-glutamylcysteine; herbicide.  
 OS Glycine max.  
 PN WO200121770-A2.  
 PD 29-MAR-2001.  
 PF 18-SEP-2000; 2000WO-GB003573.  
 PR 21-SEP-1999; 99GB-00022346.  
 PA (ZENE ) ZENECA LTD.  
 PI Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I;  
 PI Skipsey M;  
 DR WPI; 2001-257978/26.  
 DR N-PSDB; AAF57526.  
 PT Novel glutathione-S-transferase and homoglutathione synthetase sequences  
 PT from soybean for producing plants which are resistant and tolerant to  
 PT herbicide comprising fomesafen and/or acifluorfen.  
 PS Disclosure; Page 59-60; 64pp; English.

CC The invention relates to new soybean glutathione-S-transferase (GST) and  
 CC a homoglutathione synthetase (HGS). The HGS is capable of catalyzing the  
 CC addition of beta-alanine onto gamma-glutamylcysteine. Polynucleotides  
 CC encoding the proteins of the invention are useful for producing plants  
 CC which are resistant and/or tolerant to a herbicide comprising fomesafen  
 CC and/or acifluorfen. Methods of the invention are useful for providing  
 CC plants with further desired agronomic trait, especially resistant to a  
 CC herbicide, comprising glyphosate or its salt. Further desired agronomic  
 CC traits include insect resistance, nematode resistance, stress tolerance,  
 CC altered field, altered nutritional value, altered quality or any other  
 CC desirable agronomic trait. GST or its variant is also useful as a  
 CC selectable marker gene. The present sequence represents a Glycine max  
 CC clone SE3.03B09 sequence. The GST 3.3 protein sequence of the invention

CC is specifically claimed to be not a part of the present sequence

XX Sequence 234 AA;

Query Match 83.7%; Score 1000.5; DB 4; Length 234;  
 Best Local Similarity 84.6%; Pred. No. 1.1e-97;  
 Matches 192; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DLRLGAWFSPFALRVQIALNLKGLDYEVVETLNPKSELLKSNPVHKKIPVFFHGDV 64  
 Db 6 DLKLLGWFSPFALRVQIALNLKGLDYEVVETLNPKSDLLKSNPVHKKIPVFFHGDV 65

Qy 65 ICESAIIIVEYIDEVMSNNALSIIPQAYDRANARFWYSYIDDKWLTSLKSVLATEDDEAK 124  
 Db 66 ICESAIIIVEYIDEAWT-NVPSILPQAYDRANARFWAYIDEKWFTSLRSVLVAEDDEAK 124

Qy 125 KLHFEQAEVLEKVEEVFNKSEKAYFGGDTIGFVDFGSGFLSFIRVSENMMERKLLD 184  
 Db 125 KPHEQAEGLERLEEVFNKSEKAYFGGDSIGFIDIGFSGFLSWRVIEEMSGRKLLD 184

Qy 185 ETKYPGLTLWAETFAADPAVKGILPETEKLVEFAKILQLKWAATAAA 231  
 Db 185 EKKHPGLTQWAEETFAADPAVKGILPETDKLVEFAKILQLKWTATAAA 231

RESULT 7  
 ABB90937  
 ID ABB90937 standard; protein; 227 AA.  
 AC ABB90937;  
 DT 31-MAY-2002 (first entry)  
 DE Herbicidally active polypeptide SEQ ID NO 148.  
 KW Herbicidal; plant; agriculture; herbicide.  
 OS Arabidopsis thaliana.  
 PN WO200210210-A2.  
 PD 07-FEB-2002.  
 PF 28-AUG-2001; 2001WO-EP009892.  
 PR 28-AUG-2001; 2001WO-EP009892.  
 PA (FARB ) BAYER AG.  
 PI Tietjen K, Weidler M;  
 DR WPI; 2002-269010/31.  
 PT Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms.  
 PS Claim 5; SEQ ID NO 148; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
 CC for herbicidally active compounds, comprising aligning and comparing  
 CC nucleic acid or amino acid sequences from plant with nucleic acid or  
 CC amino acid sequences from non-plant organisms using suitable search  
 CC parameters, where plant sequences having an E-value greater by a factor  
 CC of 3 than the E-value of most similar non-plant sequences are selected.  
 CC The polypeptides or nucleic acids encoding them are useful for  
 CC identifying modulators. The identified modulators are useful as  
 CC herbicides

XX Sequence 227 AA;

Query Match 53.4%; Score 638; DB 5; Length 227;

Best Local Similarity 54.3%; Pred. No. 3.7e-59;  
Matches 120; Conservative 34; Mismatches 67; Indels 0; Gaps 0;

QY 1 MAERDLRLGAWFSPFALRVOIALNLKGLDYEVVVEETLNPKSELLKSNPVHKKIPVFFH 60  
DB 1 MATEDVLKIGSWASVYVMRARIALHLSISYEFLEQTYGSKSELLKSNPNVHKKMPVLIH 60  
QY 61 GDKVICSALIVEIDVWNSNLSILPONAYDRANARFWVSYYDDKWLTSKSLVLATED 120  
DB 61 ADKPVCSNIIIVHIDWNSNLSILPSPHYDRAIARFWAAYIDDQWFISVRSILTAQG 120  
QY 121 DEAKLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTGFVDIGFSGFLSFIRVSENMMNER 180  
DB 121 DEEKAALAEVEERTKLEKAFNDCSGKPFNGDHIGYLDIALGSLGWRVVELDANH 180  
QY 181 KLDDETPYGLTLWAETFAADPAVKGLLPETEKLVFEPAKIL 221  
DB 181 KFLDETPTSLVKAERFCDDPAVKPIMPEITTKLAEPARKL 221

RESULT 8  
AAB47340  
ID AAB47340 standard; protein; 233 AA.  
AC AAB47340;  
XX  
DT 19-SEP-2001 (first entry)  
XX  
DE GST3.  
XX  
KW Glutathione-S-transferase; GST; opium poppy; conjugation; herbicide;  
KW electrophilic compound; glutathione; GSH; detoxification; xenobiotic;  
KW transgenic plant; stress resistance; pathogen; grazing pest.  
XX  
OS Pavaver somniferum.  
XX  
PN WO200153501-A2.  
XX  
PD 26-JUL-2001.  
XX  
PP 18-JAN-2001; 2001WO-IB000205.  
XX  
PR 18-JAN-2000; 2000US-0176708P.  
XX  
PA (FACC/) FACCHINI P J.  
XX  
PI Facchini PJ;  
XX  
DR WPI; 2001-457612/49.  
XX  
DR N-PSDB; AAC86194.  
XX  
PT Glutathione-S-transferase polypeptide(s) useful for producing transgenic  
XX plants comprising resistance to biotic and abiotic stress.  
PS Claim 1; Page 10; 77pp; English.  
XX

This sequence shows a glutathione-S-transferase (GST) polypeptide, GST3, from the opium poppy. GST's catalyse the conjugation of electrophilic compounds to glutathione (GSH). They have been shown to be involved in detoxification of xenobiotics. The novel GST's of the invention GST1, GST2 and GST3, show extensive homology with tau type GST's from a variety of plant species, especially within the N-terminal region. This domain has been shown to be responsible for recognition of GSH and the ability of the proteins to form dimers. The C-terminal domain is responsible for substrate specificity and varies greatly between other GST's. The GST's of the invention exhibit strong glutathione conjugating activity towards a model substrate, 1-chloro-2,4-dinitrobenzene that could be inhibited in the presence of hydroxycinnamic acid amines of tyramine. The expression of the GST polypeptide in a transgenic plant is useful to produce a plant which has increased stress resistance. The plant has increased resistance to pathogens, herbicides or grazing pests. The GST polypeptide is useful to identify binding agents inhibitors and substrates

SQ Sequence 233 AA;  
Query Match 52.2%; Score 624; DB 4; Length 233;  
Best Local Similarity 54.0%; Pred. No. 1.2e-57;  
Matches 116; Conservative 39; Mismatches 60; Indels 0; Gaps 0;

QY 5 DLRLGAWFSPFALRVOIALNLKGLDYEVVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
DB 8 EVKILGWPSPFVWRPRIALNLSKVYLLLEETFGSKSELLKSNPIYKIPVMIHGDV 67  
QY 65 ICSALIVEIDVWNSNLSILPONAYDRANARFWVSYYDDKWLTSKSLVLATEDDEAK 124  
DB 68 ICESMIIVQYIDVWASAGHSIIPSDPDASIAFWATYIDDKFFPSLMGIASKDAEEK 127  
QY 125 KLHFEQAEVLEKVEEVFNKCSGKAYFGGDTTGFVDIGFSGFLSFIRVSENMMNERKLLD 184  
DB 128 KAAIEQIAAFAGLEAYQKTSKGFBEKIGYIDIAFGCYIGWIRVTEKMGKILFD 187  
QY 185 ETKYPGLTLWAETFAADPAVKGLLPETEKLVFEPAK 219  
DB 188 ETKVPLTKWAEKFCADETVKSVMPEIDALMEFAK 222

RESULT 9  
AAB47339  
ID AAB47339 standard; protein; 233 AA.  
XX  
AC AAB47339;  
XX  
DT 19-SEP-2001 (first entry)  
XX  
DE GST2.  
XX  
KW Glutathione-S-transferase; GST; opium poppy; conjugation; herbicide;  
KW electrophilic compound; glutathione; GSH; detoxification; xenobiotic;  
KW transgenic plant; stress resistance; pathogen; grazing pest.  
XX  
OS Pavaver somniferum.  
XX  
PN WO200153501-A2.  
XX  
PD 26-JUL-2001.  
XX  
PP 18-JAN-2001; 2001WO-IB000205.  
XX  
PR 18-JAN-2000; 2000US-0176708P.  
XX  
PA (FACC/) FACCHINI P J.  
XX  
PI Facchini PJ;  
XX  
DR WPI; 2001-457612/49.  
XX  
DR N-PSDB; AAC86193.  
XX  
PT Glutathione-S-transferase polypeptide(s) useful for producing transgenic  
XX plants comprising resistance to biotic and abiotic stress.  
PS Claim 1; Page 9; 77pp; English.  
XX

This sequence shows a glutathione-S-transferase (GST) polypeptide, GST2, from the opium poppy. GST's catalyse the conjugation of electrophilic compounds to glutathione (GSH). They have been shown to be involved in detoxification of xenobiotics. The novel GST's of the invention GST1, GST2 and GST3, show extensive homology with tau type GST's from a variety of plant species, especially within the N-terminal region. This domain has been shown to be responsible for recognition of GSH and the ability of the proteins to form dimers. The C-terminal domain is responsible for substrate specificity and varies greatly between other GST's. The GST's of the invention exhibit strong glutathione conjugating activity towards a model substrate, 1-chloro-2,4-dinitrobenzene that could be inhibited in the presence of hydroxycinnamic acid amines of tyramine. The expression of the GST polypeptide in a transgenic plant is useful to produce a plant which has increased stress resistance. The plant has increased resistance to pathogens, herbicides or grazing pests. The GST polypeptide is useful to identify binding agents inhibitors and substrates

CC to pathogens, herbicides or grazing pests. The GST polypeptide is useful  
 CC to identify binding agents inhibitors and substrates  
 XX  
 SQ Sequence 233 AA;

Query Match 52.1%; Score 623; DB 4; Length 233;  
 Best Local Similarity 54.0%; Pred. No. 1.5e-57;  
 Matches 116; Conservative 39; Mismatches 60; Indels 0; Gaps 0;  
 QY 5 DLRLGAWFSPFALRVOIALNLKGLDYEVVEETLNPKSELLKSNPVHKKIPVFFHGDV 64  
 DB 8 EVKILGWSPFVWPRFRIALNLIKVKYLLBETFGSKSELLKSNPIYKKMPVLIHGDV 67  
 QY 65 ICESAIIVEYIDEVWSNNALSILPQNAIDRANARFWVSYYIDDKWLTSLSKVLATEDDEAK 124  
 DB 68 ICESMIIVQYIDVWASAGHSIIIPSDPYDASIRFWATYIDDKFPFSLMGIAKSKDAEEK 127  
 QY 125 KLHFEQAEVLEKVEEVFNKSEKAYFGGDTIGFVDIGFSGFLSFTRVSENMMERKLLD 184  
 DB 128 KAAIEQAIARFGILEEAYQKTSKGDFGGEKIGYVDIAFGCYVGWIRVTEKMGIKLFD 187  
 QY 185 ETKYVGLTLWAETFAADPAVKGLLPETEKLVFAK 219  
 DB 188 EKVPLGLTKWAEKFCADETVKSVMPTDALMEFAK 222

RESULT 10  
 AAB47341  
 ID AAB47341 standard; protein; 233 AA.  
 XX  
 AC AAB47341;  
 XX  
 DT 19-SEP-2001 (first entry)  
 XX  
 DE GST consensus sequence.  
 XX  
 KW Glutathione-S-transferase; GST; opium poppy; conjugation; herbicide;  
 KW electrophilic compound; glutathione; GSH; detoxification; xenobiotic;  
 KW transgenic plant; stress resistance; pathogen; grazing pest.  
 XX  
 OS Pavaver somniferum.

XX Key Location/Qualifiers  
 FH Misc-difference 58  
 FT /label= Met, Ile  
 FT Misc-difference 61  
 FT /label= Met, Leu  
 FT Misc-difference 158  
 FT /label= Gly, Glu  
 FT Misc-difference 163  
 FT /label= Val, Ile  
 FT Misc-difference 171  
 FT /label= Val, Ile  
 FT Misc-difference 189  
 FT /label= Glu, Thr

XX WO200153501-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 18-JAN-2001; 2001WO-IB000205.  
 XX  
 XX 18-JAN-2000; 2000US-0176708P.

XX (FACC/) FACCHINI P J.  
 XX  
 XX Facchini PJ;  
 XX  
 XX WPI; 2001-457612/49.  
 XX

XX Glutathione-S-transferase polypeptide(s) useful for producing transgenic  
 PT plants comprising resistance to biotic and abiotic stress.  
 XX  
 XX

PS Claim 1; Page 12; 77pp; English.

XX This sequence shows a consensus glutathione-S-transferase (GST)  
 CC polypeptide from the opium poppy. GST's catalyse the conjugation of  
 CC electrophilic compounds to glutathione (GSH). They have been shown to be  
 CC involved in detoxification of xenobiotics. The novel GST's of the  
 CC invention GST1, GST2 and GST3, show extensive homology with tau type  
 CC GST's from a variety of plant species, especially within the N-terminal  
 CC region. This domain has been shown to be responsible for recognition of  
 CC GSH and the ability of the proteins to form dimers. The C-terminal domain  
 CC is responsible for substrate specificity and varies greatly between other  
 CC GST's. The GST's of the invention exhibit strong glutathione conjugating  
 CC activity towards a model substrate, 1-chloro-2,4-dinitrobenzene that  
 CC could be inhibited in the presence of hydroxycinnamic acid amines of  
 CC tyramine. The expression of the GST polypeptide in a transgenic plant is  
 CC useful to produce a plant which has increased stress resistance. The  
 CC plant has increased resistance to pathogens, herbicides or grazing pests.  
 CC The GST polypeptide is useful to identify binding agents inhibitors and  
 CC substrates

XX Sequence 233 AA;

Query Match 50.8%; Score 607; DB 4; Length 233;  
 Best Local Similarity 53.0%; Pred. No. 7.7e-56;  
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 DB 8 EVKILGWSPFVWPRFRIALNLIKVKYLLBETFGSKSELLKSNPIYKKMPVLIHGDV 67  
 QY 65 ICESAIIVEYIDEVWSNNALSILPQNAIDRANARFWVSYYIDDKWLTSLSKVLATEDDEAK 124  
 DB 68 ICESMIIVQYIDVWASAGHSIIIPSDPYDASIRFWATYIDDKFPFSLMGIAKSKDAEEK 127  
 QY 125 KLHFEQAEVLEKVEEVFNKSEKAYFGGDTIGFVDIGFSGFLSFTRVSENMMERKLLD 184  
 DB 128 KAAIEQAIARFGILEEAYQKTSKGDFGGEKIGYVDIAFGCYVGWIRVTEKMGIKLFD 187  
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 DB 188 EKVPLGLTKWAEKFCADETVKSVMPTDALMEFAK 222

RESULT 11  
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 AC ABB91390;  
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 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 601.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.

XX WO200210210-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 XX 28-AUG-2001; 2001WO-EP009892.  
 XX  
 XX 28-AUG-2001; 2001WO-EP009892.

XX (FARB ) BAYER AG.  
 XX  
 XX Tietjen K, Weidler M;  
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 XX WPI; 2002-269010/31.  
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XX Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 XX







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DT	17-OCT-2000 (first entry)				
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 31219.				
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KW	termination sequence.				
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XX	EP1033405-A2.				
PN	06-SEP-2000.				
XX	25-FEB-2000; 2000EP-00301439.				
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 22-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 46.7%; Score 558; DB 3; Length 233;
Best Local Similarity 48.4%; Pred. No. 1.2e-50;
Matches 106; Conservative 42; Mismatches 69; Indels 2; Gaps 2;

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Db 1 MGEREEVKLGTWSPVVRKIALRLKSVYDYVEEDLFGSKSELLKSNPIFKVPVL 60

Qy 59 FHGDKVICESAIIVEYIDEVMSNNALSILPONAYDRANARFWVSYYDDKWLTSLSKVLAT 118
Db 61 IHNTKPCVCSLNIVEYIDETWSSGSSILPSHPYDRALARFWSVFVDDKWLPTLMAAWVA 120

Qy 119 EDDEAKKLHFQAEVLEKVEEVNKCSEKAYFGGDTIGFVDFGSGFSLFIRVSENNM 178
Db 121 KSEEAkakgMBEVEGLQLQLEAAFTALSkgkSFFGGETIGFDICLGSFLVLLKAREKLK 180

Qy 179 ERKLDETKYPCLTLWAETFAADPAVKGLLPETEKLVF 217
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
10129.558 Million cell updates/sec

Title: US-10-088-945A-14  
Perfect score: 918  
Sequence: 1 cataaaactccacatttcct.....aatatagtaaaaaaaaaa 918

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 11: gb\_sts.\*
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- 15: em\_ba.\*
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- 19: em\_mu.\*
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- 22: em\_ov.\*
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- 27: em\_sts.\*
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- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	918	100.0	918	6 AX100331	AX100331 Sequence
2	620.2	67.6	895	6 AR123130	AR123130 Sequence
3	620.2	67.6	895	6 AR124082	AR124082 Sequence
4	620.2	67.6	895	6 AX100355	AX100355 Sequence
5	620.2	67.6	895	6 AF243360	AF243360 Glycine m
6	288	31.4	896	6 AX203249	AX203249 Sequence
7	288	31.4	896	8 AF118926	AF118926 Papaver s
8	270	29.4	998	6 AX203245	AX203245 Sequence
9	270	29.4	998	8 AF118924	AF118924 Papaver s
10	268.4	29.2	947	6 AX203247	AX203247 Sequence
11	268.4	29.2	947	8 AF118925	AF118925 Papaver s
12	265.4	28.9	962	8 AY091102	AY091102 Arabidops
13	264.8	28.8	988	8 AF159229	AF159229 Gossypium
14	264.4	28.8	988	8 AF288191	AF288191 Arabidops
15	263.8	28.7	964	8 AB039930	AB039930 Arabidops
16	241.6	26.3	715	8 BT000940	BT000940 Arabidops
17	240	26.1	684	6 AX507981	AX507981 Sequence
18	240	26.1	684	8 AF288190	AF288190 Arabidops
19	232.2	25.3	705	6 AX507963	AX507963 Sequence
20	231.4	25.2	938	8 AF370480	AF370480 Arabidops
21	204.2	22.2	855	8 AF177944	AF177944 Petrosali
22	197.4	21.5	866	8 AY084992	AY084992 Arabidops
23	193.6	21.1	513	6 AX506970	AX506970 Sequence
24	185.6	20.2	624	8 AF288192	AF288192 Arabidops
25	184.4	20.1	593	8 AF064201	AF064201 Gossypium
26	184	20.0	810	6 AX653837	AX653837 Sequence
27	182.4	19.9	1151	8 AK107435	AK107435 Oryza sat
28	181.8	19.8	684	6 AX506000	AX506000 Sequence
29	181.8	19.8	684	8 AF288193	AF288193 Arabidops
30	181.8	19.8	684	8 AY094051	AY094051 Arabidops
31	181.8	19.8	754	8 AY044324	AY044324 Arabidops
32	181.8	19.8	901	8 AY050343	AY050343 Arabidops
33	181.2	19.7	702	6 AX653944	AX653944 Sequence
34	181.2	19.7	928	8 AK073944	AK073944 Oryza sat
35	181.2	19.7	929	8 AK061304	AK061304 Oryza sat
36	181.2	19.7	943	8 AY271620	AY271620 Oryza sat
37	181.2	19.7	947	8 AF309379	AF309379 Oryza sat
38	179	19.5	705	8 BT006220	BT006220 Arabidops
39	179	19.5	927	8 AK119143	AK119143 Arabidops
40	178.6	19.5	1040	6 AX100349	AX100349 Sequence
41	178.6	19.5	1040	8 AF051214	AF051214 Picea mar
42	178.4	19.4	696	6 AX652944	AX652944 Sequence
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ALIGNMENTS

RESULT 1	AX100331	AX100331	918 bp	DNA	linear	PAT 10-APR-2001
LOCUS	AX100331	Sequence 14 from Patent WO0121770.				
DEFINITION	AX100331					
ACCESSION	AX100331					
VERSION	AX100331.1	GI:13619349				
KEYWORDS		Glycine max (soybean)				
SOURCE		Glycine max				
ORGANISM		Glycine max				
		Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
		rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;				
		Glycine.				
REFERENCE	1					
AUTHORS		Andrews,C.J., Jepson,I., Townson,J.K., Edwards,R., Cummins,I.D. and				

Skipsey, M.D.  
Gst sequences from soybean and their use in the production of  
herbicide resistant plants  
Patent: WO 0121770-A 14 29-MAR-2001;  
ZENECA LIMITED (GB)  
Location/Qualifiers  
1. .918  
/organism="Glycine max"  
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ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;  
Best Local Similarity 100.0%; Pred. No. 8.4e-205;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATAAACTCCACATTTTCCTGCTGAGTAACCTAACAAACAAACACACATATTGCTCCGTG 60  
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Qy 61 TTGACCTGTTATAGTAAACAGTGATGCTGAAAGGACCTTGAGGCTTTTGGGTGCTTGG 120  
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Db |||||||  
Qy 121 TTCAGTCCATTTGCCCTGAGGGTGCAGATTGCCCTTAACTCAAGGGTTTGGATTATGAG 180  
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Qy 181 GTTGTGAAGAGACTTTGAATCCCAAAAGTGAATGCTTCTTAAGTCCAAACCTTGTGCAC 240  
Db |||||||  
Qy 181 GTTGTGAAGAGACTTTGAATCCCAAAAGTGAATGCTTCTTAAGTCCAAACCTTGTGCAC 240  
Db |||||||  
Qy 241 AAGAAATCCAGTTTCTTCCATGAGATAAAGTCAATATGTAATCGCAATCATAGTT 300  
Db |||||||  
Qy 241 AAGAAATCCAGTTTCTTCCATGAGATAAAGTCAATATGTAATCGCAATCATAGTT 300  
Db |||||||  
Qy 301 GAGTACATAGATGAGTTTGTGCCAAACAAAGCTCTCTCCATCTTCCACAAATGCAATAT 360  
Db |||||||  
Qy 301 GAGTACATAGATGAGTTTGTGCCAAACAAAGCTCTCTCCATCTTCCACAAATGCAATAT 360  
Db |||||||  
Qy 361 GATCGAGTAAATGCCCGATTTTGGGTTCTTACATCGATGACAGTGGCTTACGTCCTTG 420  
Db |||||||  
Qy 361 GATCGAGTAAATGCCCGATTTTGGGTTCTTACATCGATGACAGTGGCTTACGTCCTTG 420  
Db |||||||  
Qy 421 AAAAGTGTCTAGCGACTGAAGATGATGAGGCAAGAGCTACACTTTTGACCAAGCGGAA 480  
Db |||||||  
Qy 421 AAAAGTGTCTAGCGACTGAAGATGATGAGGCAAGAGCTACACTTTTGACCAAGCGGAA 480  
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Qy 481 GAAGTGTCTGAGAAGTGGAAAGAGTGTTCACCAAGTGCAGTGAAGGGAAGGCTATTTC 540  
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Qy 541 GGAGGAGATACGATTTGGATTGTCATTTGGTTTGGAGCTTTTGGAGTTTCATTAGA 600  
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Qy 601 GTCTCAGAGATATGAATGAAGAAATTTGCTTGATGAAGCAAGTACCTGGTTTGACC 660  
Db |||||||  
Qy 661 CTATGGGCTGAACTTTTGCTGCTGATCTGCTGTGAAGGGCTTCTGCCAGAGACTGAA 720  
Db |||||||  
Qy 721 AAGCTTGTGATTTGCAAGATTTCTCAGCTAAATGGGGTGTCTGCGAGCTGCTGCAAG 780  
Db |||||||  
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Qy 781 TAAATGGAATCAAAATTAATTCGTGATGAAATTTCAAAAATTTGTTGCAAGTATTATATA 840  
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Qy 781 TAAATGGAATCAAAATTAATTCGTGATGAAATTTCAAAAATTTGTTGCAAGTATTATATA 840  
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Qy 841 TCTGAGGCTATGTTTGTGCAACTTTATATATTTAAAGTCAAAATAAATTTATATGATA 900  
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Db 901 TATAGTAAAAAAGAAAAA 918

RESULT 2  
AR123130  
LOCUS AR123130 895 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 7 from patent US 6168954.  
ACCESSION AR123130  
VERSION AR123130.1 GI:14108096  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 895)  
AUTHORS McGonigle, B. and O'Keefe, D.P.  
TITLE Soybean glutathione-S-transferase enzymes  
JOURNAL Patent: US 6168954-A 7 02-JAN-2001;  
FEATURES Location/Qualifiers  
source 1. .895  
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ORIGIN

Query Match 67.6%; Score 620.2; DB 6; Length 895;  
Best Local Similarity 88.0%; Pred. No. 6.4e-135;  
Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

Qy 97 GACTTGAGGCTTTTGGGTGCTTGTTTCAGTCCCAATTTGCCCTGAGGGTGCAGATTGCCCTT 156  
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Qy 51 GACTTGAAGCTTTTGGGAGGCTGGTTCAGCCCATTTGCCCTGAGGGTGCAGATTGCCCTT 110  
Db |||||||  
Qy 157 AACCTCAAGGGTTTGGATTATGAGGTTGTTGAAGAGACTTTGAATCCCAAAAGTGAATTG 216  
Db |||||||  
Qy 111 AACCTCAAGGGTCTAGAATATGAGGTTGTTGAAGAGACCTTGAATCCCAAAAGTGACCTG 170  
Db |||||||  
Qy 217 CTTCCTTAAGTCCCAACCTGTGCACAGAAATCCAGTTTCTTCCATGAGATGAAAGTC 276  
Db |||||||  
Qy 171 CTTCCTTAAGTCCCAACCTGTGCACAGAAATCCAGTTTCTTCCATGAGATGAAAGTC 230  
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Db |||||||  
Qy 231 ATTTGTGAATCTGCAATCATAGTTGAGTACATGATGAGGCTTGG---ACTAATGTTCCC 287  
Db |||||||  
Qy 337 TCCATCCTTCCACAAATGATATGATCGAGCTTAATGCCCGATTTTGGGTTTCTTACATC 396  
Db |||||||  
Qy 288 TCCATCCTTCCACAAATGCTTATGATCGTGAATGCTCGATTTTGGTTTGGCTACATT 347  
Db |||||||  
Qy 397 GATGACAAGTGGCTTAGCTCTTGAAGTGTCTAGGACTGAAGATGATGAGGCAAG 456  
Db |||||||  
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Db |||||||  
Qy 457 AAGCTTACACTTTGAGCAAGCGGAAGAGTGTCTGAGAAGGTGGAAGAGTGTTCACCAAG 516  
Db |||||||  
Qy 408 AAGCCACACTTTGAGCAAGCAGAGAGGCTTGAGAGGTTGGAAGAGTGTTCACCAAG 467  
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Qy 577 GGAAGCTTTTGTGATTTTCATTAGATCTCAGAGATATGATGAAGAAATTCCTTGAT 636  
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Db 767 TTTTCAAAAATGTTGTCAGAGTATTATATCTCAGGCTATGTTTGTGCAACTTTATAT 825  
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LOCUS ARI124082 895 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 7 from patent US 6171839.  
ACCESSION ARI124082  
VERSION ARI124082.1 GI:14109443  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 895)  
AUTHORS McGonigle,B. and O'Keefe,D.P.  
TITLE Soybean glutathione-S-transferase enzymes  
JOURNAL Patent: US 6171839-A 7 09-JAN-2001;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 67.6%; Score 620.2; DB 6; Length 895;  
Best Local Similarity 88.0%; Pred. No. 6.4e-135;  
Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

Qy 97 GACTTGAGCTTTTGGGAGCTTGTTCAGTCCATTTGCCCTGAGGCTGCAGATTGCCCTT 156  
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Db 171 CTTCTTAAGTCCAAACCTGTCACAGAAATCCAGTTTCTCCATGGAGATAAAGTC 230  
Qy 277 ATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGTTTGGTCCCAAAAGTGAATTG 336  
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Qy 337 TCCATCTCTCCCAAAATGCTATATGATCGTGAATGCTGATTTGGTTTGGCTTACATT 396  
Db 288 TCCATCTCTCCCAAAATGCTATATGATCGTGAATGCTGATTTGGTTTGGCTTACATT 347  
Qy 397 GATGCAAGTGGCTTACGCTTGAAGAGTGTCTAGCGACTGAGATGATGAGGCAAG 456  
Db 348 GATGAGAGTGGTTTACGCTTGAAGAGTGTCTAGTGGCTGAGATGATGAGGCAAG 407  
Qy 457 AAGCTTACACTTTGACCAAGCGCAAGTGTCTGAGAGGTTGGAAGAGTGTCTCAACAG 516  
Db 408 AAGCCACACTTTGACCAAGCGCAAGTGTCTGAGAGGTTGGAAGAGTGTCTCAACAG 467  
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Qy 577 GGAAGCTTTTTCAGTTTCATTAGAGTCTCAGAGAAATATGAAATGAAGAAATTCGCTGAT 636

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RESULT 4  
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LOCUS AX100355 895 bp DNA linear PAT 10-APR-2001  
DEFINITION Sequence 38 from Patent WO0121770.  
ACCESSION AX100355  
VERSION AX100355.1 GI:13619371  
KEYWORDS Glycine max (soybean)  
SOURCE Glycine max  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
REFERENCE 1  
AUTHORS Andrews,C.J., Jepson,I., Townson,J.K., Edwards,R., Cummins,I.D. and Skipsey,M.D.  
TITLE Gat sequences from soybean and their use in the production of herbicide resistant plants  
JOURNAL Patent: WO 0121770-A 38 29-MAR-2001;  
ZENECA LIMITED (GB)  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 67.6%; Score 620.2; DB 6; Length 895;  
Best Local Similarity 88.0%; Pred. No. 6.4e-135;  
Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

Qy 97 GACTTGAGCTTTTGGGAGCTTGTTCAGTCCATTTGCCCTGAGGCTGCAGATTGCCCTT 156  
Db 51 GACTTGAAGCTTTTGGGAGCTTGTTCAGTCCATTTGCCCTGAGGCTGCAGATTGCCCTT 110  
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Db 288 TCCATCCTTCCACAAAATGCTTATGATGCTGCTCAATGCTCGATTTGGTTGCTCATATT 347  
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Db 408 AAGCCACACTTTGAGCAAGCAGAAAGAGGGCTTGAGAGGTGGAAGAAGTGTCCAAAG 467  
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Db 468 TACAGTGAAGGAAGGCTATTTCGGAGGAGATAGCATTTGGATTCAATTTGGTTTT 527  
Qy 577 GGAAGCTTTTGGAGTTTCATTAGAGTCTCAGAGAAATATGAATGAAGAAATTCCTTGAT 636  
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RESULT 5  
AF243360 895 bp mRNA linear PLN 28-NOV-2000  
LOCUS  
DEFINITION Glycine max glutathione S-transferase GST 5 mRNA, complete cds.  
ACCESSION AF243360  
VERSION AF243360.1 GI:11385424

KEYWORDS  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

REFERENCE  
AUTHORS McConigle,B., Keeler,S.J., Lau,S.M., Koeppe,M.K. and O'Keefe,D.P.  
TITLE A genomics approach to the comprehensive analysis of the glutathione S-transferase gene family in soybean and maize  
JOURNAL Plant Physiol. 124 (3), 1105-1120 (2000)  
MEDLINE 20532786  
PUBMED 11080288

REFERENCE  
AUTHORS McConigle,B. and O'Keefe,D.P.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-2000) AgBiotechnology, DuPont, PO Box 80402, Wilmington, DE 19880-0402, USA

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RESULT 6  
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LOCUS

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DEFINITION Sequence 5 from Patent WO0153501.
ACCESSION AX203249
VERSION AX203249.1 GI:15392619
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Papaver.
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REFERENCE
AUTHORS Facchini, P.J.
TITLE Glutathione-S-transferase nucleic acids and polypeptides and
methods of use thereof
JOURNAL Patent: WO 0153501-A 5 26-JUL-2001;
Facchini, Peter James (CA)
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Best Local Similarity 59.6%; Pred. No. 5.7e-57;
Matches 486; Conservative 0; Mismatches 330; Indels 0; Gaps 0;
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RESULT 7
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LOCUS AF118926 896 bp mRNA linear PLN 02-JAN-2000
DEFINITION Papaver somniferum glutathione S-transferase 3 mRNA, complete cds.
ACCESSION AF118926
VERSION AF118926.1 GI:6652873
KEYWORDS
SOURCE
ORGANISM Papaver somniferum (opium poppy)
Papaver somniferum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Papaver.
1 (bases 1 to 896)
Facchini, P.J. and Yu, M.
Molecular cloning and characterization of a glutathione
S-transferase gene family from opium poppy
Unpublished
2 (bases 1 to 896)
Facchini, P.J. and Yu, M.
Direct Submission
TITLE Submitted (11-JAN-1999) Biological Sciences, University of Calgary,
2500 University Drive NW, Calgary, Alberta T2N 1N4, Canada
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ORIGIN
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Best Local Similarity 59.6%; Pred. No. 5.7e-57;
Matches 486; Conservative 0; Mismatches 330; Indels 0; Gaps 0;
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LOCUS AX203245 998 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 1 from Patent WO0153501.  
ACCESSION AX203245  
VERSION AX203245.1 GI:15392617

KEYWORDS Papaver somniferum (opium poppy)  
SOURCE Papaver somniferum  
ORGANISM Papaver somniferum  
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Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
Papaveraceae; Papaver.

REFERENCE 1  
AUTHORS Facchini,P.J.  
TITLE Glutathione-S-transferase nucleic acids and polypeptides and  
methods of use thereof  
JOURNAL Patent: WO 0153501-A 1 26-JUL-2001;  
Facchini, Peter James (CA)

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RESULT 9  
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DEFINITION Papaver somniferum glutathione S-transferase 1 mRNA, complete cds.  
ACCESSION AF118924  
VERSION AF118924.1 GI:6652869

KEYWORDS Papaver somniferum (opium poppy)  
SOURCE Papaver somniferum  
ORGANISM Papaver somniferum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
Papaveraceae; Papaver.

REFERENCE 1 (bases 1 to 998)  
AUTHORS Facchini,P.J. and Yu,M.  
TITLE Molecular cloning and characterization of a glutathione  
S-transferase gene family from opium poppy

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 998)  
AUTHORS Facchini,P.J. and Yu,M.  
TITLE Direct Submission

JOURNAL Submitted (11-JAN-1999) Biological Sciences, University of Calgary,  
2500 University Drive NW, Calgary, Alberta T2N 1N4, Canada

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Best Local Similarity 63.6%; Pred. No. 9.6e-53;
Matches 411; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

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RESULT 10.
AX203247
LOCUS
DEFINITION
Sequence 3 from Patent WO0153501.
ACCESSION
AX203247
VERSION
AX203247.1 GI:15392618
KEYWORDS
Papaver somniferum (opium poppy)
SOURCE
Papaver somniferum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Papaver.
REFERENCE
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AUTHORS
Facchini, P.J.

TITLE
Glutathione-S-transferase nucleic acids and polypeptides and
methods of use thereof
JOURNAL
Patent: WO 0153501-A 3 26-JUL-2001;
Facchini, Peter James (CA)
FEATURES
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Best Local Similarity 63.5%; Pred. No. 2.3e-52;
Matches 410; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

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Qy 577 GGAAGCTTTTGGATTTTCAATAGAGTCTCAGAGAAATATGAATGAAGAAAAATTCGTTGAT 636
Db 528 GGGTGTATGTTGGCTGATTTAGAGTTACAGAGAGATGAACGGAATCAAACTATTGAT 587

Qy 637 GAAACGAGTACCTGTTTACCTATGGCTGAAACTTTTGTGCTGATGATGATGATGATGAT 696
Db 588 GAAGAAAAGTTCAGGCTTACAAAATGGGCTGAGAAAATTTTGTGCTGATGAGACAGTT 647

Qy 697 AAGGGCTTCTGCCAGAGACTGAAAGCTTTGTTGAGTTTGCAAAAGA 742
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RESULT 11
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LOCUS
DEFINITION
Papaver somniferum glutathione S-transferase 2 mRNA, complete cds.
ACCESSION
AF118925
VERSION
AF118925.1 GI:6652871
KEYWORDS
Papaver somniferum (opium poppy)
SOURCE
Papaver somniferum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Papaver.
REFERENCE
1
(bases 1 to 947)
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AUTHORS Facchini,P.J. and Yu,M.  
TITLE Molecular cloning and characterization of a glutathione  
S-transferase gene family from opium poppy  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 947)  
Facchini,P.J. and Yu,M.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-1999) Biological Sciences, University of Calgary,  
2500 University Drive NW, Calgary, Alberta T2N 1N4, Canada  
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Best Local Similarity 63.5%; Pred. No. 2.3e-52;  
Matches 410; Conservative 0; Mismatches 236; Indels 0; Gaps 0;  
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DEFINITION Arabidopsis thaliana 962 bp mRNA sequence.  
ACCESSION AY091102  
VERSION AY091102.1 GI:20268697  
KEYWORDS Full cDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 962)  
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,  
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,  
Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,  
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,  
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,  
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,  
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.  
Arabidopsis Full Length cDNA Clones  
Unpublished  
TITLE Arabidopsis Full Length cDNA Clones  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 962)  
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,  
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,  
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,  
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Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,  
Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,  
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.  
Direct Submission  
SUBMITTED (20-MAR-2002) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,  
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
Hayashizaki,Y. and Shinozaki,K.  
The Salk, Stanford, PGE (SSP) Consortium members carried out the  
sequencing and annotation of the RAPL cDNAs: Yamada,K., Banh,J.,  
Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,  
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,  
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,  
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,  
Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,  
Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.  
Yamada,K. (SSP/PGE) and Seki,M. (RIKEN GSC) contributed equally to  
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGE)  
contributed equally to this work as PIs.  
Annotation is based on the January 2002 version of the Arabidopsis  
genome submitted to GenBank.  
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Best Local Similarity 61.5%; Pred. No. 1.1e-51;
Matches 425; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

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AF159229
LOCUS AF159229 988 bp mRNA linear PLN 03-FEB-2000
DEFINITION Gossypium hirsutum glutathione S-transferase mRNA, complete cds.
ACCESSION AF159229
VERSION AF159229.1 GI:6856102
KEYWORDS Gossypium hirsutum (upland cotton)
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 988)
Kang W.H., Yamamoto,E. and Allen,D.R.
Cloning and characterization of glutathione S-transferase (GST)
gene from cotton plants (Gossypium hirsutum L. cv. Coker 312)
Unpublished
2 (bases 1 to 988)
Kang,W.H., Yamamoto,E. and Allen,D.R.
Direct Submission
Submitted (15-JUN-1999) Plant and Soil Science, Texas Tech
University, 4th and Flint, Lubbock, TX 79409, USA
JOURNAL
AUTHORS
TITLE
JOURNAL
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Query Match      28.8%; Score 264.8; DB 8; Length 988;
Best Local Similarity 64.6%; Pred. No. 1.6e-51;
Matches 430; Conservative 0; Mismatches 227; Indels 9; Gaps 2;

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Qy 227 AGGATTGCCCTGAACATCAAGTCTGTGGCCTATGAATTTCTTCAGGAGAGGTTATGGAA 286
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Qy 682 GCTGATCCTGCTGTAAGGGCTTTCTGCCAGAGACTGAAAAGCTGTGTGAGTTTGCAGAA 741
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Db 821 ATGCTT 826

RESULT 14
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LOCUS Arabidopsis thaliana chromosome 1 glutathione S-transferase (GST30)
DEFINITION mRNA, complete cds.
ACCESSION AF288191
VERSION AF288191.1 GI:11096015
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 684)
REFERENCE Wagner,U. and Mauch,F.
AUTHORS Analysis of the glutathione S-transferase family in Arabidopsis
thaliana
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 684)
AUTHORS Wagner,U. and Mauch,F.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2000) Department of Biology, University of
Fribourg, 3, rte Albert Gockel, Fribourg CH- 1700, Switzerland
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gene
CDS
ORIGIN
Query Match 28.8%; Score 264.4; DB 8; Length 684;
Best Local Similarity 62.6%; Pred. No. 2e-51;
Matches 412; Conservative 0; Mismatches 246; Indels 0; Gaps 0;
Qy 85 ATGGCTGAAGGACTTGAGGCTTTGGTGGCTTGGTTCACTCCATTGCTCAGGGTG 144
Db 1 ATGGCAACGACGACGTGAAGCTGATCGGTGCATGGCGGAGTCCCTTTGTGATGAGGCCG 60

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Qy 145 CAGATTGCCCTTAACCTCAAGGGTTTGGATTATGAGGTTGTTGAAGAGACTTTGAATCCC 204
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RESULT 15
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LOCUS Arabidopsis thaliana ERD9 mRNA for glutathione S-transferase,
DEFINITION complete cds.
ACCESSION AB039930
VERSION AB039930.1 GI:15375407
KEYWORDS glutathione S-transferase.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Kiyose,T., Yamaguchi-Shinozaki,K. and Shinozaki,K.
AUTHORS Cloning of cDNAs for genes that are early-responsive to dehydration
TITLE stress (ERDs) in Arabidopsis thaliana L.: identification of three
ERDs as HSP cognate genes
JOURNAL Plant Mol. Biol. 25 (5), 791-798 (1994)
MEDLINE 94355652
PUBMED 8075396
REFERENCE 2 (bases 1 to 964)
AUTHORS Shinozaki,K., Yamaguchi-shinozaki,K. and Takahashi,S.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2000) Kazuo Shinozaki, RIKEN, Laboratory of Plant
Molecular Biology; 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
(E-mail:sinozaki@rtc.riken.go.jp. Tel: +81-298-36-4359)
FEATURES
Location/Qualifiers
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Job time : 3931 secs

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ORIGIN

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	620.2	67.6	895	4	AAF31575
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8	270	29.4	998	4	AA86192
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10	240	26.1	684	6	ABZ14871
11	232.2	25.3	705	6	ABZ14853
12	228.2	24.9	817	6	ABN98975
13	226.4	24.7	955	3	AA41255
14	202.2	22.0	863	3	AA51154
15	197.4	21.5	866	3	AA35433
16	193.6	21.1	513	6	ABZ13860
17	184	20.0	810	7	ADA70384
18	181.8	19.8	684	6	ABZ12890
19	181.8	19.8	881	3	AA47459
20	181.4	19.8	824	6	ABN98949
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22	178.4	19.4	696	7	ADA69491
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24	172.2	18.8	881	3	AA34181
25	171	18.6	834	7	ADA69909
26	167.4	18.2	970	3	AA76274
27	166.2	18.1	895	2	AAZ07557
28	166.2	18.1	895	3	AAZ94797
29	166.2	18.1	895	3	AA76262
30	164	17.9	1068	3	AA76287
31	160.4	17.5	702	7	ADA70385
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33	156.8	17.1	1143	3	AA38593
34	156	17.0	960	3	AA76279
35	152.4	16.6	934	3	AA76278
36	152	16.6	708	7	ADA69765
37	142.6	15.5	900	3	AA76281
38	142.6	15.5	926	2	AAZ5151
c	39	142.2	736	8	ACL25466
40	140	15.3	841	3	AA59485
41	139.8	15.2	860	3	AA76271
42	138.4	15.1	840	4	AAF57512
c	43	133.8	653	8	ACL25409
c	44	132.2	642	8	ACL25401
c	45	131.8	754	8	ACL25435

## ALIGNMENTS

RESULT 1  
AAF57513  
ID AAF57513 standard; DNA; 918 BP.  
XX  
AC AAF57513;  
XX  
DT 11-JUN-2001 (first entry)  
XX  
DE Glycine max glutathione-S-transferase (GST) 3.3 encoding DNA.  
XX  
KW Soybean; glutathione-S-transferase; GST; homogluthathione synthetase; HGS;  
KW beta-alanine; gamma-glutamylcysteine; herbicide; ds.  
XX  
OS Glycine max.  
XX  
FH Key Location/Qualifiers  
FT CDS 85..783  
FT /\*tag= a  
FT /product= "GST 3.3"  
XX  
PN WO200121770-A2.  
XX  
PD 29-MAR-2001.  
XX  
PF 18-SEP-2000; 2000WO-GB003573.  
XX  
PR 21-SEP-1999; 99GB-00022346.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I;  
PI Skipsey M;  
DR WPI; 2001-257978/26.  
DR P-PSDB; AAB62226.  
XX  
XX Novel glutathione-S-transferase and homogluthathione synthetase sequences from soybean for producing plants which are resistant and tolerant to herbicide comprising fomesafen and/or acifluorfen.  
XX  
PS Claim 4; Page 47; 64pp; English.  
XX  
CC The invention relates to new soybean glutathione-S-transferase (GST) and a homogluthathione synthetase (HGS). The HGS is capable of catalyzing the addition of beta-alanine onto gamma-glutamylcysteine. Polynucleotides encoding the proteins of the invention are useful for producing plants

CC which are resistant and/or tolerant to a herbicide comprising fomesafen  
CC and/or acifluorfen. Methods of the invention are useful for providing  
CC plants with further desired agronomic trait, especially resistant to a  
CC herbicide, comprising glyphosate or its salt. Further desired agronomic  
CC traits include insect resistance, nematode resistance, stress tolerance,  
CC altered field, altered nutritional value, altered quality or any other  
CC desirable agronomic trait. GST or its variant is also useful as a  
CC selectable marker gene. The present sequence represents a Glycine max GST  
CC 3.3 (also referred to as GST 3.6) protein encoding DNA  
XX  
SQ

Sequence 918 BP; 281 A; 151 C; 212 G; 274 T; 0 U; 0 Other;

Query Match 100.0%; Score 918; DB 4; Length 918;  
Best Local Similarity 100.0%; Pred. No. 1.9e-222;  
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 841 TCTGAGGCTATGTTTGTGTCGAACCTTTATATATTTAAAGTCAAAATAAATTTATGATAA 900  
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DB 901 TATAGTAAAAAATAAAAAA 918

RESULT 2

AAA53396  
ID AAA53396 standard; cDNA; 895 BP.

XX AC

XX AAA53396;  
DT 04-OCT-2000 (first entry)

XX Clone se3.03b09 nucleotide sequence encoding GST type III.

XX Soybean; glutathione-S-transferase; GST; detoxify; herbicide; stress;  
KW transgenic plant; tolerant; plant breeding; ss.

XX Glycine max.

XX US6063570-A.

XX 16-MAY-2000.

XX 05-SEP-1997; 97US-00924747.

XX 05-SEP-1997; 97US-00924747.

XX (DUPO ) DU PONT DE NEMOURS & CO S I.

PI Megonigle B, O'keefe DP;

XX WPI; 2000-375487/32.

DR P-PSDB; AAB03734.

XX New Glutathione-S-Transferase enzymes and isolated nucleic acid fragments  
encoding them, useful for detoxifying xenobiotic compounds in plants and  
seeds, as well as in producing transgenic plants that are herbicide-  
resistant.

PS Claim 2; Col 33-36; 36pp; English.

XX This sequence was isolated from a soybean clone, and encodes a  
XX Glutathione-S-Transferase (GST). The invention relates to isolated  
XX nucleic acid fragments (see AAA53393-A53406) which encode soybean GST  
XX polypeptides (AAB03731-B03744). GSTs are a family of enzymes which  
XX catalyse the conjugation of glutathione, homogluthathione and other  
XX glutathione-like analogues, to a large range of hydrophobic,  
XX electrophilic compounds. GSTs have been implicated in the detoxification  
XX of certain herbicides. The GST nucleotide sequences are useful in the  
XX construction of herbicide-tolerant transgenic plants, plants that are  
XX tolerant to a wide variety of stresses, or plants in which the GST  
XX enzymes are present at higher or lower levels than they are normally. The  
XX nucleic acid fragments are also useful as probes for genetically and  
XX physically mapping the genes that they are part of, and as markers for  
XX traits linked to expression of the enzymes. This will be useful in plant  
XX breeding in order to develop lines with desired phenotypes or in the  
XX identification of mutants. The soybean GST enzymes are used to detoxify  
XX xenobiotic compounds in plants and seeds. The enzymes are also useful as  
XX targets to facilitate design and/or identify inhibitors of the enzymes  
XX that may be used as herbicides or herbicide synergists. The GST enzymes  
XX produced in the host cells, particularly in microbial host cells, are  
XX useful in preparing antibodies to the enzymes. These antibodies are  
XX useful for detecting the enzymes in situ in cells or in vitro in cell  
XX extracts

SQ Sequence 895 BP; 260 A; 146 C; 215 G; 274 T; 0 U; 0 Other;

Query Match 67.6%; Score 620.2; DB 3; Length 895;  
Best Local Similarity 88.0%; Pred. No. 5.4e-147;

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Qy	157	AACCTCAAGGCTTTGGATATGAGTTTGTGAAGAGACTTTGAATCCCAAAAGTGAATG	216
Db	111	AACCTCAAGGCTTTAGAAATATGAGTTTGTGAAGAGACTTTGAATCCCAAAAGTGAATG	170
Qy	217	CTTCTTAAGTCCAAACCTCTGTGCAAGAAATCCAGTCTTTCTTCCATGGAGATAAAGTC	276
Db	171	CTTCTTAAGTCCAAACCTCTGTGCAAGAAATCCAGTCTTTCTTCCATGGAGATAAAGTC	230
Qy	277	ATATGTGAATCTGCAATCATAGTTAGTACATAGATGAGTTTGGTCCCAATGCTCTC	336
Db	231	ATTTGTGAATCTGCAATCATAGTTAGTACATAGATGAGTTTGGTCCCAATGCTCTC	287
Qy	337	TCCATCTCTCCAAATATGATGCTGCTTATGATGCTGCTTATGCTGCTGCTTATGCTGCT	396
Db	288	TCCATCTCTCCAAATATGATGCTGCTTATGATGCTGCTTATGCTGCTGCTTATGCTGCT	347
Qy	397	GATGACAAAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	456
Db	348	GATGACAAAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	407
Qy	457	AAGTACACATCTTGAAGAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	516
Db	408	AAGTACACATCTTGAAGAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	467
Qy	517	TGCAAGTGAAGGAGGCTTATTTGGAGGAGATACGATGCTGCTTGTGATGCTGCTGCTGCT	576
Db	468	TACAGTGAAGGAGGCTTATTTGGAGGAGATACGATGCTGCTTGTGATGCTGCTGCTGCT	527
Qy	577	GGAGCTTTTGTAGTCTTCAATGAGTCTCAGAGATATGAATGAAGAAATGCTTGTAT	636
Db	528	GGAGCTTTTGTAGTCTTCAATGAGTCTCAGAGATATGAATGAAGAAATGCTTGTAT	587
Qy	637	GAACGAAAGTACCTGCTTGAACCTATGAGGCTGAAATCTTGTGCTGCTGCTGCTGCTG	696
Db	588	GAACGAAAGTACCTGCTTGAACCTATGAGGCTGAAATCTTGTGCTGCTGCTGCTGCTG	647
Qy	697	AAGGCTCTTCCAGAGACTGAAAGCTTGTGAGTTGCAAGATATGCAAGATCTTCACTAAA	756
Db	648	AAGGCTCTTCCAGAGACTGAAAGCTTGTGAGTTGCAAGATATGCAAGATCTTCACTAAA	707
Qy	757	TGGCTGCTGCA-----GCTGCTGCAAGTAAATGGAATCAAAATTAATGCTGCTGAA	810
Db	708	TGGCTGCTGCAAGCTGCAAGCTGCAAGTAAATGGAATCAAAATTAATGCTGCTGAA	766
Qy	811	TTTCAAAATTTGTTGCAAGTATTTATATCTCAGGCTATGTTTGTGCAACTTTATAT	870
Db	767	TTTCAAAATTTGTTGCAAGTATTTATATCTCAGGCTATGTTTGTGCAACTTTATAT	825
Qy	871	ATTTAAAGTCAAAATTAATGTTATGATAATATATGATAAATAA 913	
Db	826	ATTTAAAGTCAAAATTAATGTTATGATAATATATGATAAATAA 868	

## RESULT 3

AAZ94952

ID AAZ94952 standard; cDNA; 895 BP.

XX AC AAZ94952;

XX AC AAZ94952;

XX 01-AUG-2000 (first entry)

DT Soybean glutathione-S-transferase cDNA clone se3.03B09.

DE DE

XX DE

XX KW

KW Soybean; glutathione-S-transferase; GST; xenobiotic; detoxification;

XX transgenic plant; herbicide tolerance; ss.

XX OS

OS Glycine max.

XX	Key	Location/Qualifiers
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PD		06-APR-2000.
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PF		30-SBP-1998; 98WO-US020501.
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PR		30-SBP-1998; 98WO-US020501.
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PA		(DUPO ) DU PONT DE NEMOURS & CO E I.
XX		
PI		Mcgonigle B, O'keefe DP;
XX		
DR		WPI; 2000-317517/27.
DR		P-PSDB; AAY79515.
XX		
PT		Nucleic acids encoding soybean glutathione-S-transferase enzymes useful
PT		for conferring herbicide resistance to plants.
XX		
PS		Claim 2; Page 45; 76pp; English.
XX		
CC		The present sequence is that of the cDNA insert in clone se3.03B09
CC		encoding soybean class III glutathione-S-transferase (GST, see AAY79515).
CC		The clone was isolated from a cDNA library prepared from soybean embryo.
CC		The invention provides soybean GST enzymes (see AAY79512-25) involved in
CC		the detoxification of xenobiotic compounds, especially herbicides, in
CC		plants and seeds. Chimeric genes encoding all or a portion of soybean GST
CC		enzymes, host cells, and methods of recombinant production of soybean GST
CC		enzymes are provided. The sequences are useful in the construction of
CC		herbicide-tolerant transgenic plants, in the recombinant production of
CC		GST enzymes, in the development of screening assays to identify compounds
CC		inhibitory to the GST enzymes (useful as herbicides or herbicide
CC		synergists), and in screening assays to identify chemical substrates of
CC		the GSTs
XX		
SQ		Sequence 895 BP; 260 A; 146 C; 215 G; 274 T; 0 U; 0 Other;

Query Match 67.6%; Score 620.2; DB 3; Length 895;

Best Local Similarity 88.0%; Pred. No. 5.4e-147;

Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

Qy	97	GACTTGAAGCTTTTGGGTGCTTGCTTCAATTCAGTCCCTGAGGTCAGATTCGCCCTT	156
Db	51	GACTTGAAGCTTTTGGGTGCTTGCTTCAATTCAGTCCCTGAGGTCAGATTCGCCCTT	110
Qy	157	AACCTCAAGGCTTTGGATATGAGTTTGTGAAGAGACTTTGAATCCCAAAAGTGAATG	216
Db	111	AACCTCAAGGCTTTAGAAATATGAGTTTGTGAAGAGACTTTGAATCCCAAAAGTGAATG	170
Qy	217	CTTCTTAAGTCCCAACCTCTGTGCAAGAAATCCAGTCTTTCTTCCATGGAGATAAAGTC	276
Db	171	CTTCTTAAGTCCCAACCTCTGTGCAAGAAATCCAGTCTTTCTTCCATGGAGATAAAGTC	230
Qy	277	ATATGTGAATCTGCAATCATAGTTAGTACATAGATGAGTTTGGTCCCAATGCTCTC	336
Db	231	ATTTGTGAATCTGCAATCATAGTTAGTACATAGATGAGTTTGGTCCCAATGCTCTC	287
Qy	337	TCCATCTCTCCAAATATGATGCTGCTTATGATGCTGCTTATGCTGCTGCTTATGCTGCT	396
Db	288	TCCATCTCTCCAAATATGATGCTGCTTATGATGCTGCTTATGCTGCTGCTTATGCTGCT	347
Qy	397	GATGACAAAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	456
Db	348	GATGACAAAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	407
Qy	457	AAGTACACATCTTGAAGAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	516
Db	408	AAGTACACATCTTGAAGAGTGGCTTACGCTCTTGAAGAGTCTTCTAGTGGTGAAGATGATGAGGCAAG	467



AAF31575  
 ID AAF31575 standard; DNA; 895 BP.  
 AC AAF31575;  
 XX  
 XX 09-APR-2001 (first entry)  
 DT Soybean type III GST cDNA #2.  
 DE  
 XX Soybean; glutathione-S-transferase; herbicide; GST; ds.  
 KW  
 XX Glycine max.  
 XX US6171839-B1.  
 XX 09-JAN-2001.  
 XX 22-APR-1999; 99US-00296715.  
 XX 05-SEP-1997; 97US-00924747.  
 PR (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 XX Mcgonigle B, O'keefe DP;  
 XX WPI; 2001-136874/14.  
 XX Novel soybean glutathione-S-transferase enzymes useful as targets to  
 PT facilitate design and/or identification of inhibitors of the enzyme, that  
 PT are used as herbicides or herbicide synergists.  
 XX  
 XX Claim 2; Col 33-36; 37pp; English.  
 XX  
 XX The present invention relates to soybean glutathione-S-transferase  
 CC proteins. The novel sequences are useful in the construction of herbicide  
 CC tolerant transgenic plants, in the recombinant production of glutathione-  
 CC S-transferase (GST) enzymes, in the development of screening assays to  
 CC identify compounds inhibitory to the GST enzymes, and in screening assays  
 CC to identify chemical substrates of the GSTs  
 XX  
 XX Sequence 895 BP; 260 A; 146 C; 215 G; 274 T; 0 U; 0 Other;  
 SQ  
 Query Match 67.6%; Score 620.2; DB 4; Length 895;  
 Best Local Similarity 88.0%; Pred. No. 5.4e-147;  
 Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;  
 97 GACTTGAAGCTTTTGGGAGGCTGTTGCTCAGTCCATTTCCTGAGGGTGCAGATTGCCCTT 156  
 51 GACTTGAAGCTTTTGGGAGGCTGTTGCTCAGTCCATTTCCTGAGGGTGCAGATTGCCCTT 110  
 157 AACCTCAAGGTTTGGATTATGAGGTTGTTGAAGAGACTTTGAATCCCAAAAGTGAATTG 216  
 111 AACCTCAAGGTTTGAATATGAGGTTGTTGAAGAGACTTTGAATCCCAAAAGTGAATTG 170  
 217 CTTCTTAAGTCCAAACCTGTGCAAGAATAATCCAGTTTCTTCATGAGAGATAAAGTC 276  
 171 CTTCTTAAGTCCAAACCTGTGCAAGAATAATCCAGTTTCTTCATGAGAGATAAAGTC 230  
 277 ATATGTCGAATCTGAATCATAGTTGAGTACATGAGGTTTGGTCCCAATGCTCTC 336  
 231 ATTTGTGAATCTGAATCATAGTTGAGTACATGAGGTTTGGTCCCAATGCTCTC 287  
 337 TCCATCTTCCAAAATATGATATGATGAGTAAATGCCGATTTTGGGTTTCTTACATC 396  
 288 TCCATCTTCCAAAATATGATATGATGAGTAAATGCCGATTTTGGGTTTCTTACATC 347  
 397 GATGACAAGTGGCTTACGCTCTTGAAGAGTGTCTAGCGATGAAGATGATGAGGCAAG 456  
 348 GATGAGAAGTGGTTTACGCTCTTGAAGAGTGTCTAGTGGCTGAAGATGATGAGGCAAG 407  
 457 AAGCTACACTTTGAGCAAGCGGAGAGAGTGTCTAGAGAGTGGAGAGTGTTCACCAAG 516  
 408 AAGCCACACTTTGAGCAAGCGGAGAGAGTGTCTAGAGAGTGGAGAGTGTTCACCAAG 467

517 TGCAGTGAAGGGAAGCCCTATTTCGAGGAGATACGATTGGATTGTTGACATTTGTTTTT 576  
 468 TACAGTGAAGGGAAGCCCTATTTCGAGGAGATAGCATTTGGATTCAATGACATTTGTTTTT 527  
 577 GGAAGCTTTTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 636  
 528 GGGAGCTTCTTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 587  
 637 GAAACGAAGTACCTCGTTTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 696  
 588 GAAACGAAGTACCTCGTTTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 647  
 697 AAGGGCTTCTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 756  
 648 AAGGGCTTCTTCAGTTTTCATTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTGAT 707  
 757 TGGGCTGCTGCA-----GCTGCTGCAAGTAAATGGAATCAAAATTAATTTGCTTGATGAA 810  
 708 TGGGCTGCTGCAAGTAAATGGAATCAAAATTAATTTGCTTGATGAA 868  
 811 TTTCAAAAATTTGCTTGATGAAATGGAATCAAAATTAATTTGCTTGATGAA 870  
 767 TTTTCAAAAATTTGCTTGATGAAATGGAATCAAAATTAATTTGCTTGATGAA 825  
 871 ATTTAAAGTCAAAATTAATGGAATCAAAATTAATTTGCTTGATGAA 913  
 826 ATTTAAAGTCAAAATTAATGGAATCAAAATTAATTTGCTTGATGAA 868

RESULT 6  
 AAF57526  
 ID AAF57526 standard; cDNA; 895 BP.  
 XX  
 AC AAF57526;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Glycine max clone SE3.03809 cDNA sequence.  
 XX  
 KW Soybean; glutathione-S-transferase; GST; homogluthathione synthetase; HGS;  
 KW beta-alanine; gamma-glutamylcysteine; herbicide; ss.  
 XX Glycine max.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 36..740  
 FT /\*tag= a  
 XX  
 PN WO200121770-A2.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-GB003573.  
 XX  
 PR 21-SEP-1999; 99GB-00022346.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I;  
 PI Skipsey M;  
 XX  
 XX WPI; 2001-257978/26.  
 DR P-PSDB; AAB62227.  
 XX  
 XX Novel glutathione-S-transferase and homogluthathione synthetase sequences  
 PT from soybean for producing plants which are resistant and tolerant to  
 PT herbicide comprising fomesafen and/or acifluorfen.  
 XX  
 XX Disclosure; Page 60-61; 64pp; English.  
 PS  
 XX The invention relates to new soybean glutathione-S-transferase (GST) and  
 CC a homogluthathione synthetase (HGS). The HGS is capable of catalyzing the





156 TAACCTCAAGGGTTTGGATTATGAGTTGTTGAAGAGACTTTTGAATCCCAAAAGTGAATT 215  
 141 CAACATTAATCAAGTCAAGTATTAATCTTTTGAAGAGACATTTGGTAGCAAAAGTGAAT 200  
 216 GCTTCTTAAAGTCCAAACCTGTGCAAGAAATCCCAAGTTTCTTCCATGAGAGATAAGT 275  
 201 TCTTCTGAATCAATCCTATTACAAAGAAATTCCTGTTATGATTCTATGATGAATACC 260  
 276 CATATGTAATCTGCATCATAGTTGATGATCATAGATGAGTTGGTCCAAACAATGCTCT 335  
 261 CATCTGTAATCAATGATCATTTGTTGATGATGATGATGATGATGATGATGATGATGAT 320  
 336 CTCCATCTCTCCAAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 395  
 321 TTTATCATCCGCTGATCTCTTAAGATGCTTCCATGCTGTTCTGGGCAACCTACAT 380  
 396 CGATGACAAGTGGCTTACGCTCTTGAAGAGTTTCTAGCGACTCAAGATGATGAGGCAAA 455  
 381 TGATGACAAGTTCTTCCGCTCTTAAATGGGATTCGAAGAGTAAGATGAGGAGAA 440  
 456 GAAGCTACATTTGAGCAAGCGGAGAGAGTGTCTTGAGAGGTGGAAGAGTGTTCACAA 515  
 441 AAAAGCAGCCATTGAACAGGCGATTGCGAGCTTTTGGTATCTACTGGAAGAGCTTATCAG 500  
 516 GTGCAAGTCAAGGAGGCTTATTTGCGAGGAGATACGATTTGATTTGATGATGATGAT 575  
 501 AACTAGTAAAGGAGAAAGACTTTTTCGGGAGAGAAATTTGGATACATGATATGCAAT 560  
 576 TGAAGCTTTTGTAGTTTCTATTAGAGTCTCAGAGATATGAATGAAAGAAATTTGCTGA 635  
 561 TGGTGTATATAGTTGGATAGAGTTACAGAGAAATGATGATCAAACTATTGGA 620  
 636 TGAACCAAGTACCTGCTTGGCTTACCTATGAGGCTGAAACTTTTGGCTGATCCTGCTGT 695  
 621 TGAACCAAGTACCTGAGGCTTACAAATGGGCTGAGAAATTTTGTGAGATGAGACAGT 680  
 696 GAAGGGCTCTGCGAGAGTGAAGAGTGTGAGTTGCAAGATTTCTAGCTAAA 755  
 681 TAAATCTGTTATGCTGAAACTGATGCTCTCATGGAGTTGCTTAAGAGATCTTTGATC 740  
 756 ATGGGCTGCTGACGCTGCTGCAAGTAAATGGAATCAATTAATTTGCTGGATGAATTTCA 815  
 741 TAACCTCTCTCTTCAAACTAGAAAGAGTTGTTAACAATGAAATATCTTAGAGATGTTA 800  
 816 AAAATGTTGTGCAAGTTATTTATATCTGAGGCTATGTTGTTGCAACTTTTATATATTA 875  
 801 AGCTTTGTTGTTTTCAGTGTGTTGATGCAATGCTTAAGAACTGTTTGTAGAAATG 860  
 876 AAAGTCAAAATTAATGTTATGATTAATATAGTAAAAA 911  
 861 ATCAAGAACAGTAGCTGTAAAAAAGAAAAAAGAAAAA 896

## RESULT 8

AAC86192

ID AAC86192 standard; cDNA; 998 BP.

AC AC

XX AC86192;

XX 19-SEP-2001 (first entry)

XX GST1 nucleic acid.

XX DE

XX Glutathione-S-transferase; GST; opium poppy; conjugation;

XX electrophilic compound; glutathione; GSH; detoxification; xenobiotic;

XX transgenic plant; stress resistance; pathogen; herbicide; grazing pest;

XX ss.

XX Papaver somniferum.

XX OS

XX WO200153501-A2.

XX EN

XX 26-JUL-2001.

XX PD

XX 18-JAN-2001; 2001WO-IB000205.

XX 18-JAN-2000; 2000US-0176708P.

XX (FACC/) PACCHINI P J.

XX Pacchini PJ;

XX WPI; 2001-457612/49.

XX Glutathione-S-transferase polypeptide(s) useful for producing transgenic

XX plants comprising resistance to biotic and abiotic stress.

XX Claim 2; Page 8; 77pp; English.

XX This sequence encodes a glutathione-S-transferase (GST) polypeptide, GST1

XX from the opium poppy. GST's catalyze the conjugation of electrophilic

XX compounds to glutathione (GSH). They have been shown to be involved in

XX detoxification of xenobiotics. The novel GST's of the invention GST1,

XX GST2 and GST3, show extensive homology with tau type GST's from a variety

XX of plant species, especially within the N-terminal region. This domain

XX has been shown to be responsible for recognition of GSH and the ability

XX of the proteins to form dimers. The C-terminal domain is responsible for

XX substrate specificity and varies greatly between other GST's. The GST's

XX of the invention exhibit strong glutathione conjugating activity towards

XX a model substrate, 1-chloro-2,4-dinitrobenzene that could be inhibited in

XX the presence of hydroxycinnamic acid amines of tyramine. The expression

XX of the GST polypeptide in a transgenic plant is useful to produce a plant

XX which has increased stress resistance. The plant has increased resistance

XX to pathogens, herbicides or grazing pests. The GST polypeptide is useful

XX to identify binding agents inhibitors and substrates

XX Sequence 998 BP; 336 A; 143 C; 213 G; 306 T; 0 U; 0 Other;

XX Query Match 29.4%; Score 270; DB 4; Length 998;

XX Best Local Similarity 63.6%; Pred. No. 3e-58;

XX Matches 411; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

XX 97 GACTTGAGGCTTTGGTGTCTTTCAGTCCATTTGCCCTGAGGGTGCAGATTCGCCCTT 156

XX 99 GAGTGAAGATTTTAGTGGATGGCCAAAGTCCATTTGTGATGAGGCTAGAAATTCGACTC 158

XX 157 AACCTCAAGGTTTGGATTAAGTTGTTGAAGAGACTTTGAATCCCAAAAGTGAATTG 216

XX 159 AACATTAATCAGTCAAGTATTATCTTCTTGAAGAGACATTTGGTAGCAAAAGTGAAT 218

XX 217 CTCTTAAAGTCCCAACCTGTGCAAGAAATCCAGTTTCTTCCATGAGATAAAGTC 276

XX 219 CTCTGAAATCAATCCTATTACAAAGATGCTGCTCTTGATTCAGGTGATAAACCC 278

XX 277 ATATGTAATCTGCAATCATAGTTGATGATGATGATGATGATGATGATGATGATGAT 336

XX 279 ATCTGTAATCAATGATCATTTGTTAGTACATGATGATGATGATGATGATGATGAT 338

XX 337 TCCATCTCTCCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396

XX 339 TCCATCTCTCTCTGATCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 398

XX 397 GATCACAAGTGGCTTACGCTCTTGAAGAGTTTCTAGCGACTGAAGATGATGAGGCAAG 456

XX 399 GATGACAAGTCTTCTCGTCTCTTAAATGGGATTCGAAGAGTAAAGATGAGGAGAA 458

XX 457 AAGCTACACCTTTGAGCAAGCGGAGAGAGTCTTGAAGAGTGAAGAGTGTTCACCAAG 516

XX 459 AAAGCAGCCATTGACAGGCGATTGCGAGCTTTTGGTATCTTGAAGAGCTTATCAGAA 518

XX 517 TGCAGTGAAGGAGGCTTATTTCCGAGGAGATACGATTTGGATTTGTCATTTGTTT 576

XX 519 ACTAGTAAAGGAGAAAGATTTTTCGGTGGAGAAAAATTTGGTATGTCGATTTTGCAT 578

XX 577 GGAAGCTTTTGTGATTTTCATTAGATCTCAGAGATATGATGAAGAAATTCCTTGTAT 636

Db 579 GGGTGTATGTTGGCTGATAGATTACAGAGAAGATGAACGAATCAAACTATTGAT 638  
Qy 637 GAAACGAAGTACCTGGTTGACCCCTATGGGCTGAAACTTTTGTCTGATCCTCGCTGTG 696  
Db 639 GAAGAAAAGTTCCAGGGCTTACAAAATGGGCTGAGAAATTTTGTCTGATGAGACAGATT 698  
Qy 697 AAGGCCCTTCGCAGAGACTGAAAGCTTTGAGTTTGAAGA 742  
Db 699 AAATCTGTTATGCTGAACTGATGCCCTCATGGAGTTGCTAAGA 744

RESULT 9  
AAC86193  
ID AAC86193 standard; cDNA; 947 BP.  
XX  
AC AAC86193;  
XX  
DT 19-SEP-2001 (first entry)  
XX  
XX GST2 nucleic acid.  
XX  
XX Glutathione-S-transferase; GST; opium poppy; conjugation;  
KW electrophilic compound; glutathione; GSH; detoxification; xenobiotic;  
KW transgenic plant; stress resistance; pathogen; herbicide; grazing pest;  
KW ss.  
XX  
XX Papaver somniferum.  
XX  
XX Key Location/Qualifiers  
FH 27.728  
FT CDS /\*tag= a  
FT /product= "GST2"  
XX  
XX WO200153501-A2.  
XX  
PD 26-JUL-2001.  
XX  
XX 18-JAN-2001; 2001WO-IB000205.  
XX  
XX 18-JAN-2000; 2000US-0176708P.  
XX  
XX (FACC/) FACCHINI P J.  
XX  
XX Facchini PJ;  
XX  
XX WPI; 2001-457612/49.  
XX  
XX P-PSDB; AAB47339.  
XX

Glutathione-S-transferase polypeptide(s) useful for producing transgenic plants comprising resistance to biotic and abiotic stress.

Claim 2; Page 9; 77pp; English.

This sequence encodes a glutathione-S-transferase (GST) polypeptide, GST2, from the opium poppy. GST's catalyse the conjugation of electrophilic compounds to glutathione (GSH). They have been shown to be involved in detoxification of xenobiotics. The novel GST's of the invention GST1, GST2 and GST3, show extensive homology with tau type GST's from a variety of plant species, especially within the N-terminal region. This domain has been shown to be responsible for recognition of GSH and the ability of the proteins to form dimers. The C-terminal domain is responsible for substrate specificity and varies greatly between other GST's. The GST's of the invention exhibit strong glutathione conjugating activity towards a model substrate, 1-chloro-2,4-dinitrobenzene that could be inhibited in the presence of hydroxycinnamic acid amines of tyramine. The expression of the GST polypeptide in a transgenic plant is useful to produce a plant which has increased stress resistance. The plant has increased resistance to pathogens, herbicides or grazing pests. The GST polypeptide is useful to identify binding agents inhibitors and substrates

Sequence 947 BP; 312 A; 135 C; 207 G; 293 T; 0 U; 0 Other;

Query Match 29.2%; Score 268.4; DB 4; Length 947;  
Best Local Similarity 63.5%; Pred. No. 7.5e-58;  
Matches 410; Conservative 0; Mismatches 236; Indels 0; Gaps 0;  
Qy 97 GACTTGAGGGCTTTGGGTGCTTGGTTTCAGTCCATTTGGCCCTGAGGGTGACAGATTGCCCTT 156  
Db 48 GAGGTGAAGATTTTAGTGTGATGCCAAGTCCATTTGTGATGAGGCTAGAAATTCACCTC 107  
Qy 157 AACCTCAAGGGTTTGGATTATGAGGTTTGTGAAGAGACTTTTGAATCCCAAAGTGAATTG 216  
Db 108 AACATTAATCAGTCAAGTATTATCTCTTGAAGAGACATTTGGTAGCAAAAGTGAACCT 167  
Qy 217 CTTCTTAAGTCCAAACCTGTGACAGAAATCCAGTTCTTCCATGAGAGATAAAGTC 276  
Db 168 CTTCTGAAATCAAAATCCTATTTTCAAGAAGATGCTGTCTTTGATTACGGTGATAAACCC 227  
Qy 277 ATATGTGAATCTGCAATCATAGTTGATACATAGATGAGGTTTGGTCCCAACATGCTCTC 336  
Db 228 ATCTGTGAATCAATGATCATTTGTCAGTACATTTGATGATGCTGCGGCTTCTGCTGTCAT 287  
Qy 337 TCCATCCTTCCACAAAATGCATATGATCGAGCTAATGCCCGATTTTGGGTTTCTTACATC 396  
Db 288 TCCATCATCCTTCTGATCCTTATGATGCTTCCATTGCTGTTCTGGGCAACCTACATT 347  
Qy 397 GATGACAAAGTGGCTTAGTCCCTTGAAGAGTGTCTTAGCGACTGAAGATGATGAGGCAAG 456  
Db 348 GATGACAAAGTCTTTCGCTCTTTAATGGGGATTGCAAGAGATGAAGATGCAAGAAGAAA 407  
Qy 457 AAGCTACACTTTCAGCAAGCGGAAGATGCTCTTGAGAAGGTGGAAGAGTGTCAACAAG 516  
Db 408 AAAGAGCCATTAAGACAGGCGATTGACGCTTTTGTGATATCTTGAAGAGCTTATCAGAAA 467  
Qy 517 TGCAGTGAAGGAGGCGCTAATTTCCGAGGAGATACGATTTGGATTGTGTGATTTGTTT 576  
Db 468 ACTAGTAAGGAAAGATTTTTCGGTGGAGAAAAATTCGGTATGTCGATATTGCAATT 527  
Qy 577 GGAAGCTTTTGTGATTTCAATGAGCTCAGAGAAATGATGAATGAAGAAAAATTCCTTGAT 636  
Db 528 GGGTGTATTGTTGGCTGGATTAGAGTTACAGAGAAGATGAACGGAATCAAACTATTTTGAT 587  
Qy 637 GAAACGAAGTACCTGTTTGACCCCTATGGCTGAACTTTTGTGCTGATCCTGCTGTG 696  
Db 588 GAAGAAAAAGTTCAGGGCTTACAAAATGGGCTGAGAAATTTGTGCAGATGAGACGTT 647  
Qy 697 AAGGGCTTCTGCCAGAGACTGAAAAGCTTTGTTGAGTTTGCAAAAGA 742  
Db 648 AAATCTGTATGCTGAACTGATGCCCTCATGGAGTTTGCCTAAGA 693

RESULT 10  
ABZ14871  
ID ABZ14871 standard; DNA; 684 BP.  
XX  
AC ABZ14871;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2676.  
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX  
PN WO200216655-A2.  
XX  
PD 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-US026685.  
PF 24-AUG-2000; 2000US-0227866P.  
XX 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX







PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.	Query Match	24.7%;	Score 226.4;	DB 3;	Length 955;
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.	Best Local Similarity	58.7%;	Pred. No. 3.3e-47;		
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.	Matches 411;	Conservative	0;	Mismatches 286;	Indels 3; Gaps 1;
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.					
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.					
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.					
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160768P.					
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.					
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.					
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.					
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.					
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.					
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.					
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.					
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.					
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.					
PR	27-JUL-1999;	99US-0145919P.	PR	25-OCT-1999;	99US-0161359P.					
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.					
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.					
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.					
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.					
PR	03-AUG-1999;	99US-0146703P.	PR	28-OCT-1999;	99US-0161992P.					
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.					
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.					
PR	05-AUG-1999;	99US-0147192P.								
PR	05-AUG-1999;	99US-0147260P.								
PR	06-AUG-1999;	99US-0147303P.								
PR	06-AUG-1999;	99US-0147416P.								
PR	09-AUG-1999;	99US-0147493P.								
PR	09-AUG-1999;	99US-0147935P.								
PR	10-AUG-1999;	99US-0148171P.								
PR	11-AUG-1999;	99US-0148319P.								
PR	12-AUG-1999;	99US-0148341P.								
PR	13-AUG-1999;	99US-0148565P.								
PR	13-AUG-1999;	99US-0148684P.								
PR	16-AUG-1999;	99US-0149368P.								
PR	17-AUG-1999;	99US-0149175P.								
PR	18-AUG-1999;	99US-0149426P.								
PR	20-AUG-1999;	99US-0149722P.								
PR	20-AUG-1999;	99US-0149723P.								
PR	20-AUG-1999;	99US-0149929P.								
PR	23-AUG-1999;	99US-0149902P.								
PR	23-AUG-1999;	99US-0149930P.								
PR	25-AUG-1999;	99US-0150566P.								
PR	26-AUG-1999;	99US-0150884P.								
PR	27-AUG-1999;	99US-0151065P.								
PR	27-AUG-1999;	99US-0151066P.								
PR	27-AUG-1999;	99US-0151080P.								
PR	30-AUG-1999;	99US-0151303P.								
PR	31-AUG-1999;	99US-0151338P.								
PR	01-SEP-1999;	99US-0151930P.								
PR	07-SEP-1999;	99US-0152363P.								
PR	10-SEP-1999;	99US-0153070P.								
PR	13-SEP-1999;	99US-0153758P.								
PR	15-SEP-1999;	99US-0154018P.								
PR	16-SEP-1999;	99US-0154039P.								
PR	20-SEP-1999;	99US-0154779P.								
PR	22-SEP-1999;	99US-0155113P.								
PR	23-SEP-1999;	99US-0155486P.								
PR	24-SEP-1999;	99US-0155659P.								
PR	28-SEP-1999;	99US-0156458P.								
PR	29-SEP-1999;	99US-0156596P.								
PR	04-OCT-1999;	99US-0157117P.								
PR	05-OCT-1999;	99US-0157753P.								
PR	06-OCT-1999;	99US-0157865P.								
PR	07-OCT-1999;	99US-0158029P.								
PR	08-OCT-1999;	99US-0158232P.								
PR	12-OCT-1999;	99US-0158369P.								
PR	13-OCT-1999;	99US-0159293P.								
PR	13-OCT-1999;	99US-0159294P.								
PR	13-OCT-1999;	99US-0159295P.								
PR	14-OCT-1999;	99US-0159329P.								
PR	14-OCT-1999;	99US-0159330P.								
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Best Local Similarity 57.3%; Pred. No. 7.le-40;	
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#### SUMMARIES

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8	157.6	17.2	904	3	US-09-248-335-69
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#### ALIGNMENTS

##### RESULT 1

US-08-924-747-7  
; Sequence 7, Application US/08924747  
; Patent No. 6063570  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE  
; TITLE OF INVENTION: ENZYMES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
; SOFTWARE: MICROSOFT WORD VERSION 7.0A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/924,747  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FLOYD, LINDA AXAMETHY  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: CL-1108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 302-892-8112  
; TELEFAX: 302-773-0164  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 895 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: SOYBEAN  
; IMMEDIATE SOURCE:  
; CLONE: SE3.03B09  
US-08-924-747-7

Query Match 67.6%; Score 620.2; DB 3; Length 895;  
Best Local Similarity 88.0%; Pred. No. 2.8e-164;

Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

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## RESULT 2

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; Sequence 7, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; PRIOR APPLICATION NUMBER: 1999-02-10  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 7  
; LENGTH: 895  
; TYPE: DNA  
; ORGANISM: SOYBEAN  
US-09-247-373B-7

Query Match 67.6%; Score 620.2; DB 3; Length 895;  
Best Local Similarity 88.0%; Pred. No. 2.8e-164;  
Matches 724; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

QY 97 GACTTGAAGCTTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGGTGCAGATTGCCCTT 156  
DB 51 GACTTGAAGCTTTTGGGAGGCTGCTTCCAGCCATTTGCCCTGAGGGTGCAGATTGCCCTT 110

QY 157 AACCTCAAGGGTTTGGATATGAGGTTTGAAGAGACTTTTGAATCCCAAAAGTGAATTG 216  
DB 111 AACCTCAAGGGTTTGAATATGAGGTTTGAAGAGACTTTTGAATCCCAAAAGTGAATTG 170

QY 217 CTTCTTAAGTCCCAACCTGTGCACAAAGAAATCCAGTTTCTCCATGAGATAAAGTC 276  
DB 171 CTTCTTAAGTCCCAACCTGTGCACAAAGAAATCCAGTTTCTCCATGAGATAAAGTC 230

QY 277 ATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGTTTGGTCCCAACAATGCTCTC 336  
DB 231 ATTTGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGTTTGGTCCCAACAATGCTCTC 287

QY 337 TCCATCTTCCCAAAAATGCAATATGATCGAGCTTAATGCCCGATTTTGGGTTTCTTACATC 396  
DB 288 TCCATCTTCCCAAAAATGCAATATGATCGAGCTTAATGCCCGATTTTGGGTTTCTTACATC 347

QY 397 GATGACAAGTGGCTTACGTTCCGAGGAGATACGATTTGGAATTTGTTGACATTTGGTTTT 456  
DB 348 GATGACAAGTGGTTTACGTTCTTGAAGAGTGTCTAGTGGCTGAAGATGATGAGGCAAG 407

QY 457 AACCTACACTTTTCAGCAAGCGGAAGAGTGTTCAGAAAGTGAAGAGTGTTCACAAAG 516  
DB 408 AACCCACACTTTTCAGCAAGCGGAAGAGGCTTTGAGAGGTTTGAAGAGTGTTCACAAAG 467

QY 517 TGCAGTGAAGGGAAGGCTTATTTCCGAGGAGATACGATTTGGAATTTGTTGACATTTGGTTTT 576  
DB 468 TACAGTGAAGGGAAGGCTTATTTCCGAGGAGATAGCATTTGGAATTTGATTTGGTTTT 527

QY 577 GGAAGCTTTTTCAGTTCATAGAGTCTCAGAGATATGATGAAGAAATTTGCTTGAT 636  
DB 528 GGGAGCTTCTTTCAGTTCATAGAGTCTCAGAGATATGATGAAGAAATTTGCTTGAT 587

QY 637 GAAACGAAGTACCTGTTTGAACCTATGGCTGAAACTTTTGTCTGATCCTGCTGTG 696  
DB 588 GAAACGAAGTACCTGTTTGAACCTATGGCTGAAACTTTTGTCTGATCCTGCTGTG 647

QY 697 AAGGCGCTTCTGTCAGAGACTGAAAGTGTGTTGAGTTTGCAGAGATTTCTTCAGCTAAAA 756  
DB 648 AAGGCGATTTCTTCAGAGACTGATAGCTTTGAGTTTGCAGAGATTTCTTCAGCTAAAA 707

QY 757 TGGGCTGCTGCA-----GCTGCTGCAAGTAAATGGAATCAAAATTAATTTGCTGGATGAA 810  
DB 708 TGGAGTCTGTCAGAGCTGCAAGTAAATGGAATCAAAATTAATTTGCTGGATGAA-GTA 766

QY 811 TTTCAAAAATTTGTCAGGTTATTTATATCTCAGGCTATGTTTGTTCGAACCTTTATAT 870  
DB 767 TTTTCAAAAATTTGTCAGGTTATTTATATCTCAGGCTATGTTTGTTCGAACCTTTATAT 825

QY 871 ATTTAAAGTCAAAATTAATTTATGATAATATAGTAAAAA 913  
DB 826 ATTTAAAGTCAAAATTAATTTATGATAATATAGTAAAA 868

## RESULT 3

US-09-296-715-7  
; Sequence 7, Application US/09296715  
; Patent No. 6171839  
; GENERAL INFORMATION:



Db 330 AGGCGCTCTCCCGCCGACCCCTATGAACGCGCGTCTGCTCGCTTCTGGGCCAAATACG 389  
Qy 395 TCGATGACAAAGTGGCTTACGCTCTTGAAGAGTGTCTAGCGACTGAAGATGATGAGCAA 454  
Db 390 TCGACGGCAAGTTGACGGCATGATGGTGAAGGCGCTCATGGGGCAACGAGGAGGAGA 449  
Qy 455 AGAAGCTACACTTTGAGCAAGCGGAAGAGTGTCTTGAAGAGTGAAGAGTGTCAACA 514  
Db 450 GGGCGACGGCAGCGTGGACGCGCTGCGCTATGACACGCTGAGGGCGGTTTCGCCG 509  
Qy 515 AGTCAAGTGAAGGAGGCGCTATTTGCGAGAGATACGATTGGAATTTGTTGACATTTGGTT 574  
Db 510 AGTCTCGCGGGGAAAGTCTTTCGCGCGGACGCGCGCGGTACCTGACGCTCGCGC 569  
Qy 575 TTGGAAGCTTTTTCAGTGTTCATTAGTCTCAGAGATATGAATGAAGAAATTTGCTTG 634  
Db 570 TGGGAGGCTTCATCGCTGGCTGCGCGCTGGGACAGGTGGGGGGCGTCAAGCTGCTGG 629  
Qy 635 ATGAAGCAAGTACCTGTTTGAACCTATGGGCTGAAACTTTTGTGCTGATCCTGCTG 694  
Db 630 ACGCGCGCGGTCGCGCGCTGGCCAGCTGGCGGAGCGCTTCGCGCGCTCGACGTAG 689  
Qy 695 TGAAGGGCTTCTGCGAGAGACTGAAGAGCTTGTGAGTTTGAAGATTTCTTCAAGTAA 754  
Db 690 CCAAGGAGGTATCCCGGACCCGACCATCGCGGAGTTTGCCAAAGTGTCTGAGGCAC 749  
Qy 755 AATGGCTGCTGACGTCTGCTCAAGTAA 783  
Db 750 GCTCGGCGAGCTGCGCACGCACTGA 778

## RESULT 5

US-08-924-759-23  
; Sequence 23, Application US/08924759  
; Patent No. 5962229

## GENERAL INFORMATION:

; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE  
; TITLE OF INVENTION: ENZYMES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY  
; STREET: 1007 MARKET STREET  
; CITY: WILMINGTON  
; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 19898

## COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95  
; SOFTWARE: MICROSOFT WORD VERSION 7.0A

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/924,759  
; FILING DATE:

## CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FLOYD, LINDA AXAMETHY

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: CL-1128

; TELEPHONE: 302-892-8112

; TELEFAX: 302-773-0184

; INFORMATION FOR SEQ ID NO: 23:

## SEQUENCE CHARACTERISTICS:

; LENGTH: 895 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: MAIZE  
; IMMEDIATE SOURCE:  
; CLONE: CS1.PK0059.B2  
US-08-924-759-23

Query Match 18.1%; Score 166.2; DB 2; Length 895;  
Best Local Similarity 53.2%; Pred. No. 5.7e-37;  
Matches 374; Conservative 0; Mismatches 328; Indels 1; Gaps 1;

Qy 72 ATAGTAAACAGTGATGCTCAAAAGGACCTTGAAGGCTTTTGGTGTCTTGGTTCAGTCAATT 131  
Db 39 AGAGTCTATTAATGCGGACGAGCGAGCTGCGAGCTCTGGGCTCATGGTACAGCCCTA 98  
Qy 132 TGCCCTGAGGGTGCAGATTGCCCTTAACCTCAAGGGTTTCGATTATGAGGTGTTGAAGA 191  
Db 99 CGTGATCCGCGCCAGGTGGCGCTGGGGCTGAAGGGCTCAGTACGATGCTGCGAGGA 158  
Qy 192 GACTTTTGAATCCCAAAAGTGAATTGCTTTTAAAGTCCAAACCCCTGTGCAAGAAATCCC 251  
Db 159 GGACCTCTCCCGCAAGAGCGACCTGCTGCTGAAGCTCAACCCGCTGCACAGGAAGTGC 218  
Qy 252 AGTTTCTTCCATGCGAGATAAAGTCAATGATGTAATCTGCAATCATAGTTGAGTACATA 311  
Db 219 CGTGTGCTGTCACGGCGCGCCCGCTGTCGAGTCTGCTCATCTCGAGTACGTGCGA 278  
Qy 312 TGAGGTTTGTGCCAAATGCTCTCTCCATCTTCCACAAAATGCAATATGATGAGCTAA 371  
Db 279 CGAGACCTGGGAGGACCGCGGACCCCTCTCTCCCGCGCAGCGCTACGACCGCCAT 338  
Qy 372 TGCCCGATTTTGGGTTTCTTACATCGATGACAAAGTGGCTTTACGTCCTTTGAAAAGTGTCT 431  
Db 339 GGCTCGCTTCTGGGACGCTTACGTCGACGACAAGTTCTACAAGAGTGAACCGGCTGT 398  
Qy 432 AGCGACTGAAGATGATGAGCAAAAGACTACATTTTGAAGCAAGCGGAAGAGTGTGTA 491  
Db 399 CTGCTCGACGACGCGGAGGAAGGCGCGGAGGCGCTCGGCTGCTGCTCCCGCTGGTGA 458  
Qy 492 GAAGGTGGAAGAGTGTTCACAAAGTGCAGTGAAGGAAGCGCTATTTCGAGGAGATAC 551  
Db 459 GACGCTGGAGCAGCGCTTTCAGGAGTGTCTCAAAGGAA-ACCTTCTTCGCGCGCAGCG 517  
Qy 552 GATTGGAATTTTGCACATTTGGTATTTTGAAGCTTTTGGAGTTCATTAGAGTCTCAGAGAA 611  
Db 518 CGTCGGGCTCGTGACATCGCTCGGAGCTTCGTTGATGATGATGATGATGATGATGATG 577  
Qy 612 TATGAATGAAGAAATTTGCTTGAAGCAAGAGTACCTGTTGACCCCTATGGGCTGA 671  
Db 578 GCGCGCGCGGTAAAGCTTCTGGACGAGGCAAGTTCCCGGCTTGAACGCGCTGGCGGA 637  
Qy 672 AACTTTTGTGCTGATCTGCTGAGGGCTTCTGCCAGAGACTCAAAAGCTTGTGTA 731  
Db 638 GCGCTTCTTGGCGGTGAGCGCCGTAAGAGAGGTATGCCGAGCGCCGGAAGGCTGTGGA 697  
Qy 732 GTTTCAAAGATTTCTCAGCTAAAATGGGCTGCTGCAAGTCTGCT 774  
Db 698 GCACTACAAGGGTTTCTGCTAAACGGTCTCCACCTGCTGGT 740

## RESULT 6

US-09-248-335-23

; Sequence 23, Application US/09248335

; Patent No. 6096504

; GENERAL INFORMATION:

; APPLICANT: MCGONIGLE, BRIAN

; APPLICANT: O'KEEFE, DANIEL

; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES

; FILE REFERENCE: CL-1128-A

; CURRENT APPLICATION NUMBER: US/09/248,335

; CURRENT FILING DATE: 1999-02-10

; EARLIER APPLICATION NUMBER: 08/924,759

; EARLIER FILING DATE: 1997-September-05

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; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-23

```

Query Match	18.1%; Score 166.2; DB 3; Length 895;
Best Local Similarity	53.2%; Pred. No. 5.7e-37;
Matches	374; Conservative 0; Mismatches 328; Indels 1; Gaps 1;
QY	72 ATAGTAAACAGTGATGGCTGAAGGGGACTTTGAGGCTTTTGGTGCTGTGGTTTCAGTCCATT 131
Db	39 AGAGTCTAATGCGGACGAGGCGAGCTGCGCTGGCTCAGCTACGAGTTCGTGCGAGGA 98
QY	132 TGCCTCTGAGGGTGCAGATTGCCCTTAAACCTCAAGGGTTTGGATTATGAGGTTGTGAAGA 191
Db	99 CGTGATCCGCGCAAGGTGGCGCTGGGGCTGAAGGGCTCAGCTACGAGTTCGTGCGAGGA 158
QY	192 GACTTTGATATCCCAAAGTGAATGGCTTTTAAGTCCAAACCTGTGCACAAAGAAATCCC 251
Db	159 GGACCTCTCCCGCAAGACGACCTGTGCTGTAAGCTCAACCGGTGCACAGGAAGGTGCC 218
QY	252 AGTTTTCTCCATGGAGATAAAGTCATATGTGAATCTGCAATCTGCAATCTGAGTACATAGA 311
Db	219 CGTGTGGTCCAGCGCGCGCCCGTGTGCGAGTCTGCTCGTCATCTGCAGTACGTCGA 278
QY	312 TGAGGTTTGGTCCAAACAATGCTCTCTCCATCCTTCCACAAAATGCATATGATCGAGCTAA 371
Db	279 CGAGACTGGCAGGCACCGGGACCCCTCTCTCCCGCGCAGCGCTACGACCGCGCAT 338
QY	372 TGCCGATTTTGGTTTCTTACATCGATGACAAGTGGCTTACGTCCTTGGAAGTGTTCCT 431
Db	339 GGCTCGCTCTGCGCAGCTACGTCGACGACAAGTTCTACAAGAGTGGAAACCGGCTGTT 398
QY	432 AGCGACTGAAGATGATGAGGCAAGAGCTACACTTTTGACNACGGGAAGNAGTGCTTGA 491
Db	399 CTGGTTCGACGACGGCGGAGAGGCGCGGAGGCGCTCGGCGTCGTCGCCCCGTGGTGGGA 458
QY	492 GAAGGTGGAAAGAAGTGTTCAAACAGTCGAGTGAAGGGAAGCGCTTATTTTCGAGGAGATAC 551
Db	459 GACGCTGGACAGCGGTTTCAAGGAGTCTCCAAAGGGA-ACCTTCTTCGCGCGCGACGC 517
QY	552 GATTGAAATTTGACATGCGTTTGTGAAGCTTTTTCAGTTTTCATTAAGAGTCTCAGAGAA 611
Db	518 CGTCGGGCTCGTGGACATCGCGTTCGGGAGCTTCGTGGTGTGGATCAGGGTGTGGACGA 577
QY	612 TATGAATGAAGAAATTTGCTTGATGAAACGAGTACCCCTGGTTTGGACCTATGGGCTGA 671
Db	578 GCGCGCGCGCGTAAAGCTTCTGACGAGGCCAAGTTCCTCGGCGCTTGACGGCTGGGCGGA 637
QY	672 AACTTTTGTGCTGATCTCGTGTGAAGGCGCTTCTGCGAGAGACTGAAAGCTTGTGTGA 731
Db	638 GCCTTCTTGGCGGTGACGCGCGTGAAGGAGTGTATGCCGGAACCGCGAGGCTGTGGGA 697
QY	732 GTTTGCAAGATTCTTCAGCTTAAATGGGCTGTGTCAGCTGCT 774
Db	698 GCACCTAAAGGGTTTTCTGGCTAAACCGCTCTCCACCTGCTGGT 740

RESULT 7  
US-09-248-335-73  
Sequence 73, Application US/09248335  
Patent No. 6096504  
GENERAL INFORMATION:  
APPLICANT: MCGONIGLE, BRIAN  
APPLICANT: O'KEEF, DANIEL  
TITLE OF INVENTION: PLANT GLUTATHIONE  
FILE REFERENCE: CU-1128-A  
CURRENT APPLICATION NUMBER: US/09/248-335-73  
CURRENT FILING DATE: 1999-02-10  
EARLIER APPLICATION NUMBER: 08/924, 812

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; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 73
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-73

```

Query Match	17.9%	Score 164;	DB 3;	Length 1068;
Best Local Similarity	53.1%;	Pred. No. 2.6e-36;		
Matches	372;	Conservative 0;	Mismatches 325;	Indels 3; Gaps 1;
Qy	88	GCTGAAAGGACATTGAGCGTTTTGGGTGCTTGGTTTCAGTCCATTTGCCCTGAGGAGTGACAG	147	
Db	35	GGTGACGATGAACCTCAAGCTGCTGGGGCGCTGGCGAGCCCAATTCGCTCTCGGGGTGAAG	94	
Qy	148	ATTGCCCTTAACCTCAAGGGTTTTGGATTATGAGGTTGTTGAAGAGACATTGMAATCC---C	204	
Db	95	CTCGCGCTCAGCTTCAAGGGCCTGAGCTACGAGGACGTGGAGGAGGACCTCTCCGGCGGC	154	
Qy	205	AAAAGTGAATTGCTTCTTAAGTCAACCCCTGTGCACAAGAAATCCACAGATTTCTTCCAT	264	
Db	155	AAGAGCGAGCTGCTCTCTCGAGTCAACCCCGTGCACAAGAAAGGTGCCCGTCTCTCCAC	214	
Qy	265	GGAGATAAAGTCATATGTGAATCTGCAATCATAGTTGAGTGACATAGATGAGTTTGGTCC	324	
Db	215	AACGGCAAGCCTGTGTGCGAGTGCAGATCATCGTGCAGTACATCGATGAGCCTTCGCC	274	
Qy	325	AACAATGCTCTCTCCATCTCTCCACAAAATGCATATGATCGAGCTAATGCCCGATTTTGG	384	
Db	275	GGCACTGGCCGCTCCCTCTCTCCCTGCCGACCCGCACCCAGCGCGCTCGCTCTCGT	334	
Qy	385	GTTTCTTACATCGATGACAAAGTGCGTTACGTCCTTGAAAAGTGTTCTAGCGACTGAAGAT	444	
Db	335	GGTGCCCTACATTGACACAAAGCTCCTAGCCCTCTGGCTGCAATCAGCAAGGCCCAAGACG	394	
Qy	445	GATGAGCAAGAAGCTACACTTTTGACAGACGGAAGAGTGCTTGAGAGGTGCGAAGAA	504	
Db	395	CAGGAGAAAGGCCGAGGCGCTGAACGACGCGCTCGCCGCGCGAGAACCTCGAGGCC	454	
Qy	505	GTGTTCAACAAGTGCAAGTGAAGGAAAGCCCTATTTCGGAGGAGATACGATTGATTGTT	564	
Db	455	GCCTTCACGAGATCTCCGAGGCAAGCCCTCTTCGGCGCGACACGCTCGGTACTCG	514	
Qy	565	GACATTGGTTTTGGAAGCTTTTTGAGTTTCATTAGAGTCTCAGAGAATATGAATGAAGA	624	
Db	515	GACGTGACGCTGGGAGCGCTGCTCGCGTGGGTGCACGCCGCCGAGAGAAGCTGTACGGGATG	574	
Qy	625	AAATTGCTTGATGAACGAGTACCCCTGTTTGACCCCTATGGGCTGAACCTTTTGCTGCT	684	
Db	575	AGGCTCTTCACGCGCACGAGGACCCCGCGCTGAGCGCGTTCGTGGAGAGGTTCCGGCGC	634	
Qy	685	GATCCTCTCTGTAAGGGCCCTCTTGCCAGAGACTGMAAAGCTTGTTGAGTTTGCAAGATT	744	
Db	635	CTCGGAGCGCCAAAGCGGTGCTTGCCGACGTGATGGCCTCGTTCGAATACGCCAACAG	694	
Qy	745	CTTCAGCTAAAATGGGCTGTGAGCTGTGCAAGTAAA	784	
Db	695	AGCAGCGCCGACGCGGAGCTGACAGCTCGGACAGCTAAA	734	

RESULT 8  
US-09-248-335-69  
; Sequence 69, Application US/09248335  
; Patent No. 6096504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEF, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; CURRENT FILING DATE: 1999-02-10

; EARLIER APPLICATION NUMBER: 08/924,759  
; EARLIER FILING DATE: 1997-September-05  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 69  
; LENGTH: 904  
; TYPE: DNA  
; ORGANISM: maize  
US-09-248-335-69

Query Match

Best Local Similarity 17.2%; Score 157.6; DB 3; Length 904;

Matches 338; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

Qy 97 GACTTGAAGCTTTTGGGCTGCTGTTTCAGTCCATTGCTGAGGGTGCGAGATTGCGCTT 156

Db 85 GAGCTGAAGCTGCTGGGCTGTGGGACAGCCGTACGTCAACAGGGTCCAGATCGTCTC 144

Qy 157 AACCTCAAGGGTTTGGATTATGAGGTTGTTGAAGAGACTTTGAATCCCAAAGTGAATTG 216

Db 145 AACCTCAAGGGCTCAGCTACGAGTACGTGAGGAGGACCTCTCAGCAAGAGCGAGCTC 204

Qy 217 CTTCTTAAGTCCAACTGTCACAGAAATCCAGTTTCTTCCATGGAGATAAAGTC 276

Db 205 CTCCTCAATTCAAACCGGTGCACAAGAAAGTCCCGTCTCATCCACGCGCGCAAGCG 264

Qy 277 ATATGTGAATCTGCAATCATAGTTAGTACATAGATGAGGTTTGGTCCAAATGCTCTC 336

Db 265 GTCCCGAGTCGAGGCGATGTTTCAGTACCTCAGCAGGCTTCCCAGGGCACGTTT 324

Qy 337 ---TCCATCCTTCCACAAATGCAATATGATCGAGCTAATGCCGATTTTGGTTTCTTAC 393

Db 325 CCGTCCGTCTCTCCAGCGCAACCTAGCGACGCCACCGCCGCTTCTGGCGCGCTTC 384

Qy 394 ATCGATGACAGTGGCTTACGTCCTTGAAAGTGTCTAGGACACTGAAGATGAGGCA 453

Db 385 GTCGACGACAGTGGCTCTCCATGCGCACACGCTCTGTTGCGCGCGGAGCAGCGAAG 444

Qy 454 AAGAGCTACACTTTGAGCAAGCGAAGAGTGTTCGAGAGGTGGAAGAGTGTTCAC 513

Db 445 AAGCGGACGCGGCTGCGGATCGTCGCGCTGAGAGCTGAGAGGTGCGTTCGAG 504

Qy 514 AAGTGCAGTGAAGGAAGCGCTATTTCCGAGGAGATACGATTGGAATTTGACATGGT 573

Db 505 GACTGCTCCGCGGAGGAGCTACTTCCGCGGACGCCATCGGCTTCTGCGAGCTGGTC 564

Qy 574 TTTGGAAGCTTTTGAAGTTTCAATAGAGTCTCAGAGATATGAATGAAGAAATTCCTT 633

Db 565 CTCGGCAGCTACCTGGGCTGGTTCAAGGTGTTTCAGAGAGATGGTCGCGCTCAGGCTCTG 624

Qy 634 GATGAACGAAGTACCTGTTGACCTATGGCTGAAACCTTTTGTCTGTGATCTCTGCT 693

Db 625 GACGTGGGAGAGCGCGCTCTCGCCGCTGGGGGAGCGTTTCGCGCGCGCGGAAGCG 684

Qy 694 GTGAAGGCGCTTCTGCCAGA 713

Db 685 GCCAAGGACGCTCTGCCGA 704

RESULT 9

US-09-248-335-57

; Sequence 57, Application US/09248335

; Patent No. 6096504

; GENERAL INFORMATION:

; APPLICANT: MCGONIGLE, BRIAN

; APPLICANT: O'KEEF, DANIEL

; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES

; FILE REFERENCE: CL-1128-A

; CURRENT APPLICATION NUMBER: US/09/248,335

; CURRENT FILING DATE: 1999-02-10

; EARLIER APPLICATION NUMBER: 08/924,759

; EARLIER FILING DATE: 1997-September-05

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: Microsoft Word Version 7.0A

; SEQ ID NO 57

; LENGTH: 960

; TYPE: DNA

; ORGANISM: maize

US-09-248-335-57

Query Match

Best Local Similarity 17.0%; Score 156; DB 3; Length 960;

Matches 362; Conservative 0; Mismatches 325; Indels 1; Gaps 1;

Qy 92 AAAGGACCTTGAAGCTTTTGGGCTGCTGTTTCAGTCCATTGCTGAGGGTGCAGATTG 151

Db 1 AACCGCAGCTGAAGCTGCTGCGCATGTGGCGAGCCGTTTGGCTTACGGCGGAAGCTAG 60

Qy 152 CCCTTAACCTCAAGGGTTTGGATTATGAGGTGTTGAAGAGACTTTGAATCCCAAAAGTG 211

Db 61 CGCTCACTTCAAGGGCTGCTTACGAGTACGTAGAGGAGGACCTCCGACGACGAGCG 120

Qy 212 AATTGCTTTTAAGTCCAACTGTCACAAAGAAATCCCAAGTTTCTTCCATGGAGATA 271

Db 121 ACCTTCCTGCTGAGCTCGAACCCGCTGCAAGAAAGGTGCCGCTCTCATCCAAACGGCG 180

Qy 272 AAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGTTTGTCCAACTAG 331

Db 181 TGCCCGTCTGTGAGTCGCGGTCATCGTGGAGTACCTCGACGAAAGTCTACAGCGCCACGG 240

Qy 332 CTCTCTCATCTTCCACAAAATGCAATGATCGAGCTAATGCCGATTTTGGGTTTCTT 391

Db 241 GCCCGCTTCTCCCTGCGGACCCATACGAGGCTGCCATGGCGGCTTCTGGGCTCAT 300

Qy 392 ACATCGATGACAAAGTGGCTTACGTCCTTGAAAAAGTGTCTTAGCGACTGAAGATGATGAG 451

Db 301 TCATCGACGAAAAGTTCTTGGCTGCTGAAAGGCGAAGGCGCAAGCGACGAGG 360

Qy 452 CAAAGAGCTACACTTTGACCAAGCGAAGAGTGTCTTGAGAGGTGGAAGAGTGTTC 511

Db 361 AGAAGCGCGAAGGTTTGAAGCTGACACTCGCGCCGCTAGAAACCTTGAAGGGGCGTTCA 420

Qy 512 ACAAGTGCAGTGAAGGAGGCGCTATTTCGAGGAGATACGATTGGATTGTTGACATTG 571

Db 421 TGAAGTCTCAAGGGGAGCCCTTCTTGGAGGCGATGTCGCGCTACTCGACATCG 480

Qy 572 GTTTTGAAGCTTTTGAAGTTTCATTAGAGTCTCAGAGAAATGAATGAAGAAATTCG 631

Db 481 CGCTCGGGGCTTGGTAGCGTGGATGCGGCCACCGAGGCGCGTCACTGCTCAGGCTCT 540

Qy 632 TTGATGAACGAAGTACCTTGGTTTACCCCTATGGGCTGAACTTTTGTCTGCTGATCCTG 691

Db 541 TCAGCGCTCCAGAGTCCGCTGCTGGAGAA- GTGGGTGGAGCGCTTCAGCGAGCTGGAACG 599

Qy 692 CTGTGAAGGCGCTTCTGCCAGAGACTGAAAAGCTTGTGAGTTTGCAAGATTCTTCAGC 751

Db 600 AGGTGTTGGCGGTCTATGCCGAGCATCGACCGGCTAGTAGAGTCTCGGCAAGGTGAGGAGG 659

Qy 752 TAAAAATGGGCTGCTGCGAGCTGCTGCAAA 779

Db 660 CTGCTGCGGCTGCAGCAGCTGCCGTAAA 687

RESULT 10

US-09-248-335-55

; Sequence 55, Application US/09248335

; Patent No. 6096504

; GENERAL INFORMATION:

; APPLICANT: MCGONIGLE, BRIAN

; APPLICANT: O'KEEF, DANIEL

; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES

; FILE REFERENCE: CL-1128-A

; CURRENT APPLICATION NUMBER: US/09/248,335

; CURRENT FILING DATE: 1999-02-10

; EARLIER APPLICATION NUMBER: 08/924,759

; EARLIER FILING DATE: 1997-September-05



; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 55  
; LENGTH: 934  
; TYPE: DNA  
; ORGANISM: maize  
US-09-248-335-55

Query Match 16.6%; Score 152.4; DB 3; Length 934;  
Best Local Similarity 53.2%; Pred. No. 4.3e-33;  
Matches 346; Conservative 0; Mismatches 301; Indels 3; Gaps 1;  
Qy 85 ATGCTGAAAGGGACTTGAGGCTTTTGGGTCTTGGTTCAGTCCATTTGCCCTGAGGCTG 144  
Db 54 ATGTCAGAGCGCGCGTGGTGTGATCGCCCTATGCGCGAGCCCGTTCGTGATCCGCGTC 113  
Qy 145 CAGATTCGCCCTTAACCTCAAGGGTTTGGATTATGAGGTTTGTGAAGAGACTTTTGAATCCC 204  
Db 114 CTGATCGCCCTGAAGCTCAAGGGCTCGAGTTTCAGTTTCGTGGAGGAGTGGTGGCGAGG 173  
Qy 205 AAAAGTGAATTTGCTTTTAAGTCAACCCCTGTGCAAGAAATCCCAAGTTTCTTCCAT 264  
Db 174 AAGAGCGAGCTGCTGCTGAGGTGCAACCCCGTGCACAAAGATCCCGCTCTCTCTCCAC 233  
Qy 265 GGAGTAAAGTCATATGTAATCTGCAATCATATGATGATGATGATGATGATGATGATGATG 324  
Db 234 CACGGCAAGCCATCTCCGAGTCTCTGATGCTGCTCAGTACATCGACGAGGCTCTGTGCC 293  
Qy 325 AACAAATGCTCTCTCCATCTTCCACAAATATGATGATGATGATGATGATGATGATGATGATG 384  
Db 294 TCCGGCGCGCGGCTTCTCCCTCCGCTCGACGCTCAAGCCCGCGCTCCAGGCTTCTGG 353  
Qy 385 GTTCTTTACATCGATGACAGTGGCTTACGCTTGTGAAAGTGTCTTAGGCACTGAAGAT 444  
Db 354 GCGCAGTACGTCGACGCAAGCTGCTTGGGC---GATCCGCACTCTGAAGGGAACGGAC 410  
Qy 445 GATGAGCAAGAAGCTACACTTTGACCAAGCGGAAGTGTGTGAAGAGTGTGAAGAGTGAAGAA 504  
Db 411 GACGGGGGCAATGAGCAGCGCGCGGCGAGCTGTCCGCGCCCTGCAAGCTCTTAGAGGAG 470  
Qy 505 GTGTTTCAACAGTGCAGTGAAGGAGGAGGCTTATTCGGAGGAGATACATTTGATTTGTT 564  
Db 471 GCTTTTCGGCAGCTCAGCAGGGAAGCGCTACTTCGGCGGGGACAGCGTCCGTACTGTG 530  
Qy 565 GACATTTGTTTGAAGCTTTTGAAGTTTCAATTAGAGTCTCAGAGAATATGAATGAAGA 624  
Db 531 GACATCGCTCTGTTGTCATGTCTGCTGAGTGAAGCGGTGAAGAGATCGCGCGGCTC 590  
Qy 625 AAATTTGTTGATGAACGAAGTACCTGTTGACCTTATGCGCTGAAACTTTTGTCTGCT 684  
Db 591 ACCCTGCTGGAACAAGGCCAAGTCCCGAACCTGGTGGCGTGGGCTGATCGTCTGTGTGCC 650  
Qy 685 GATCCTGCTGGAAGGGCTTCTCCAGAGACTGAAAGCTTTGTTGAGTT 734  
Db 651 CACCGCGCGTGTGCGAGCCCATCCCTGACCGGACAAAGTTCTGTTGAGTT 700

RESULT 11  
US-09-248-335-61  
; Sequence 61, Application US/09248335  
; Patent No. 6096504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 08/924,759  
; EARLIER FILING DATE: 1997-September-05  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 61

; LENGTH: 900  
; TYPE: DNA  
; ORGANISM: maize  
US-09-248-335-61

Query Match 15.5%; Score 142.6; DB 3; Length 900;  
Best Local Similarity 53.3%; Pred. No. 2.4e-30;  
Matches 348; Conservative 0; Mismatches 299; Indels 6; Gaps 2;  
Qy 85 ATGCTGAAAGGGACTTGAGGCTTTTGGGTCTTGGTTCAGTCCATTTGCCCTGAGGCTG 144  
Db 28 ATGTCGAGGCGCGCTGCGAGTATCGGCTATGCGCGAGCCCGTTCGTGATCCGCGTC 87  
Qy 145 CAGATTCGCCCTTAACCTCAAGGGTTTGGATTATGAGGTTTGTGAAGAGACTTTTGAATCCC 204  
Db 88-CTGATCGCGCTGAAGCTGAAGCATGTGGAGTACAGTTCGTGGAGGAGTGGTGGGCGAGC 147  
Qy 205 AAAAGTGAATTTGCTTTTAAGTCCAACTGTGTGCACAAAGAAATCCCAAGTTTCTTCCAT 264  
Db 148 AAGAGCGAGCTGCTGCTCGGCTCGAACCCTGTCACAAAGAAATCCCGTCTCTCTCCAC 207  
Qy 265 GGAGTAAAGTCATATGTAATCTGCAATCATATGATGATGATGATGATGATGATGATGATG 324  
Db 208 CACGGCAAGCCCTCTCCGAGTCCCTAAATCATGCTTTCAGTACATCGACGAGGCTCTGTGCC 267  
Qy 325 AACATGCTC---TCTCCATCTTCCACAAATATGATGATGATGATGATGATGATGATGATGATG 381  
Db 268 TCCGGCGCGCGCGGCGCATCTCTCCCGCGAGCCCTTACCGCGCGCTGTCCAGCGGTTT 327  
Qy 382 TGGTCTTTTACATCGATGACAAAGTGGCTTACGCTCTTGAAGTGTCTTAGCGACTGAA 441  
Db 328 TGGCGCAGTACGTCGACGACAGATGACCCGCG---GATCCGCTACTGAAGGGAACG 384  
Qy 442 GATGATGAGCAAGAAGCTTACACTTTTGAAGCAAGCGGAAGTGTGTGAAGAGTGAAGAA 501  
Db 385 TACGACGGGACAAAGAGAGGAGGCGGCGGCGAGCTGTCCGCGCCCTGCACTCTCGAG 444  
Qy 502 GAAGTGTTCACAAAGTGCAGTGAAGGAGGCGCTTATTCGGAGGAGATACGATTTGAGTT 561  
Db 445 GAGGCTTTTCGCGAGCTCGGCCAGGGAAGCGCTACTTCGGCGGGGACAGCGTCCGGTAC 504  
Qy 562 GTTGACATTTGTTTGAAGCTTTTGAAGTTTCAATTAGAGTCTCAGAGAATATGAATGAA 621  
Db 505 CTGACATCCCTTGTGTGCGAGTGGTGGTGAAGGCGGTGGAGAGATCGCGGG 564  
Qy 622 AGAAATTTGTTGATGAACGAAGTACCTGTTTGAACCTATGGGCTGAAACTTTTGTCT 681  
Db 565 GTCACTCTGCTGGACGAGGCGAAGTTTCCCAACCTGGTGGCGTGGGCTGACCGGCTGTGC 624  
Qy 682 GCTGATCTGCTGAAGGCGCTTCTCCAGAGACTGAAAGCTTTGTTGAGTT 734  
Db 625 GCCCACCAGCGCGTGTGGAGCGCATCCCTGACCGCGCAAGTTCTGTTGAGTT 677

RESULT 12  
US-09-247-373B-53  
; Sequence 53, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; CURRENT FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 08/924,747  
; PRIOR FILING DATE: 1997-09-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 53  
; LENGTH: 841  
; TYPE: DNA  
; ORGANISM: SOYBEAN

US-09-247-373B-53

Query Match 15.3%; Score 140; DB 3; Length 841;  
Best Local Similarity 52.1%; Pred. No. 1.2e-29;  
Matches 367; Conservative 0; Mismatches 325; Indels 12; Gaps 2;

QY 97 GACTTGAGGCTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGGTGCAGATTGCCCTT 156  
DB 1 GAGGTGAAGCTTCATGGATTGTTGGTATAGTCCCTACACACTTTGAGGGTGGTATGACCTTA 60

QY 157 AACCTCAAGGGTGTGGATTATGAGGTGTGGAAGAGACTTTGAAATCCCAAAGTGAATTG 216  
DB 61 AAGTTAAGGATATACCATATCAAAACATGAAGAGACCGCTACAAATAGAGTCTCAA 120

QY 217 CTTCTTAAGTCCAAACCTGTGCACAAAGAAATCCAGTTTCTTCCATGGAGATAAAGTC 276  
DB 121 CTTCTTGAATACACCCAGTATACAGAAACTCCAGTGTCTTGTCCATATATGGAACCC 180

QY 277 ATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGTTTGGTCCAAATGCTCTC 336  
DB 181 TTATGTGAGTCCATGCTTATTGTTGAATACATTTGATGAGATTGGTACATAAT----- 234

QY 337 TCCATCTTCCACAAATGCATATGATCGAGCTAATGCCGATTTTGGGTTTCTTACATC 396  
DB 235 TCATTACTTCTGCTGATCCCTACGAGAGACTCTGGCAAGTTTGGGTTAAATATGCT 294

QY 397 GATGACAAAGTGGCTTACGTCCTTGAAGAGTGTCTAGCGACTGAAGATGATGAGGCAAG 456  
DB 295 GATGATGACATGTTTCTGCAAGTATTGCAATCTTCTTACCAATATGATGAAGCGA 354

QY 457 AAGCTACACTTTGAGCAAGCGGAAGAAGTGTGAGAAAGTGGGAAGAGTGTTCACAAG 516  
DB 355 GAAAGAGCATAGAGAAGATATGGGAGCATCTCAGGGTGTGTGAGAATCACT-----GT 408

QY 517 TGCATGTGAAGGAAGGCTATTTCGGAGGAGATACGATTGGATTGTTGACATTTGTTT 576  
DB 409 TTTGGTGATCAGAAGAAATTTTGGGGGAGACATTATTAACTATGGACATAGCTTTT 468

QY 577 GGAAGCTTTTGGAGTTTCATTAGAGTCTCAGAGAATATGAATGAAGAAATTCCTTGAT 636  
DB 469 GGGTCCATATTCAAAATCTTGTGTTGCAGAAGATATTCTTGACGCGAAGGTCTCGAA 528

QY 637 GAAACGAAGTACCTGTGTTGACCCCTATGGGCTGAAACTTTTGTGCTGTGATCTCTGTG 696  
DB 529 GATGAGAAATCCCTCACTTCATTCATGTTATGTTAATAATTTCAAGGATGTTGCAAGTTAT 588

QY 697 AAGGCTCTTGCAGAGACTGAAAGCTTTGAGTTTGCARAAGATCTTCAGCTAAA 756  
DB 589 AAAGAAACCTCCAGACCATGAGAAATGTTGGCTTTTGTAAAGTTATTAGAGAAAA 648

QY 757 TGGGCTGCTGCAGCTGTGCAAGTAAATGGAATCAAAATTAATT 800  
DB 649 CGTTGGCATGTACTAAGAAAGTAACTTATATGAGATCAAGT 692

RESULT 13

US-09-248-335-41  
; Sequence 41, Application US/09248335  
; Patent No. 6095504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEF, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 08/924,759  
; EARLIER FILING DATE: 1997-September-05  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 41  
; LENGTH: 860  
; TYPE: DNA

; ORGANISM: maize  
US-09-248-335-41

Query Match 15.2%; Score 139.8; DB 3; Length 860;  
Best Local Similarity 51.7%; Pred. No. 1.4e-29;  
Matches 355; Conservative 0; Mismatches 317; Indels 15; Gaps 1;

QY 96 GGACTTGAGGCTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGGTGCAGATTGCCCT 155  
DB 56 GGGTCTGACGCTGTGGGCTGCACGTCGAGCCCTTCGCTTGGCGCTGCGCATGCGCT 115

QY 156 TAACCTCAAGGTTTGGATTATGAGGTGTGGAAGAGACTTTGAAATCCCAAAGTGAATT 215  
DB 116 GAGCCTCAAGGGCTGAGCTACGAGTACATCGAGCAGGACCTGTTCACAAGGGCGAGCT 175

QY 216 GCTTCTTAAGTCCAAACCTGTGCACAAAGAAATCCCAAGTTTCTTCCATGAGATAAAGT 275  
DB 176 CTTCTCAGTCAAAACCCGTGCACAAGAGGTGCCGCTCATCCACACGCAAGCC 235

QY 276 CATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGTTTGGTCCAAATGCTCT 335  
DB 236 CATCTGAGTCCCTCGCGCTCGTGGAGTACGTCGATGAGTCTGGCCCGCGCGCGC 295

QY 336 CTCCATCTTCCAAATATGCATATGATCGAGCTAATGCCGATTTTGGGTTTCTTACAT 395  
DB 296 CACCATCTCTCCCGCGGACCCCAACGCTCGCGCACCGCTTCTGGGCGCGCTACAT 355

QY 396 CGATGACAAAGTGGCTTACGTCTTGAAGAGTGTCTAGCGACTGAAGATGATGAGGCAAA 455  
DB 356 CGACGGCAAGCTGTTCCGGCGTGGACAGGATCATGAAGCGCGGACGAGGAAGCGAG 415

QY 456 GAAGCTACACTTTGAGCAAGCGAAAGAGTGTGAGAAAGGTGGAAGAGTGTTCACAA 515  
DB 416 GGGGATAAGCTGAGGAGAGACGACGCGCGGCTCTCAACCTGGAGAAGGCTTTCGCGCA 475

QY 516 G-----TGCAGTGAAGGAAGGCTTATTTCCGAGGAGATACGATTGGAATT 560  
DB 476 GATCAGCTCTAGTCCAGCAACGACGCGCGGCTTCTTCGCGGCGACCTCCGTCGGGTA 535

QY 561 TGTGACATTTGTTTGAAGCTTTTGTAGTTTTCATTAGAGTCTCAGAGAATATGAATGA 620  
DB 536 CTTGAGCTCGCTCGGCTCGGCTGCTCCCTGCGGTGTTGGGGCGCTGCGGCCCATGCTCG 595

QY 621 AAGAAATTCCTTGTATGAAACGAAGTACCTCGTGTGACCCCTATGGGCTGAAACTTTTGC 680  
DB 596 CGTCGAGATCATCGACGCGCCAGGCTCCGCTCCTGGTGGCGTGGGCGGAGGATTTGG 655

QY 681 TGTGATCTGCTGTGAGGGCTTCTGCCAGAGACTGAAAGCTTGTGAGTTTGCAA 740  
DB 656 GAGACCCCGTGGCCCAAGAGGTGCTGCGCAGCGGACGAGGCTGTGGCCTACGCCAA 715

QY 741 GATTCTTCAGCTAAATGGGCTGCTGC 767  
DB 716 GAAGATTCAGGCTACTGGGCTTCTGC 742

RESULT 14

US-09-248-335-71  
; Sequence 71, Application US/09248335  
; Patent No. 6095504  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEF, DANIEL  
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1128-A  
; CURRENT APPLICATION NUMBER: US/09/248,335  
; CURRENT FILING DATE: 1999-02-10  
; EARLIER APPLICATION NUMBER: 08/924,759  
; EARLIER FILING DATE: 1997-September-05  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 71  
; LENGTH: 1013

```
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-71

Query Match      14.3%; Score 131.4; DB 3; Length 1013;
Best Local Similarity 55.2%; Pred. No. 3.5e-27;
Matches 280; Conservative 0; Mismatches 221; Indels 6; Gaps 1;

Qy 65 ACCTGTTATAGTAACAGTGTGGCTGAAAGGGAGCTTGGAGCTTTTGGGTGCTTGGTTCA 124
Db 83 ATCTGGAGAGGAAACAAATGCGCGCGAGGAGGCTTTAAGGTCTCTCGGCTCGAGGTGA 142
Qy 125 GTCCATTGTCCTGAGGGTGCAGATGCGCTTAACCTCAAGGGTTGGATTATCAGGTTG 184
Db 143 GCCCGTTCGTCTCCGCTGCTGCTGGCGCTGAACATGAAGAGAGTGAGTTACGATACG 202
Qy 185 TTGAAGAGACTTTGAATCCCAAGAGTGAATTTGCTTTTAACTCCAAACCCCTGTGCACAAGA 244
Db 203 TCGAGGAGGACATATCCAAACAGAGTGAGCTCTCTCAAGTCCAAACCCGCTGCACAAGA 262
Qy 245 AAATCCCAAGTTTCTTCATCGAGATAAAGTCAATGTAATCTGCAATCATATGTTGAGT 304
Db 263 AGGTGCCGTGCTCATCCACAACGTAAGCCCATCTGCGAGTCACTCGTCAATCATGCAGT 322
Qy 305 ACATAGATGAGGTTGGTCCAAACATGCTCTCTCCATCCTTCCACAAAATGCATATGATC 364
Db 323 ACCTCGACGAGCTGTTGCGCCGCG-----CGGCCGATCCTCCCAACCGACCCCTACGAGC 376
Qy 365 GAGCTAATGCGCGGATTTTGGGTGTTCTTACATCGATGACAAGTGGCTTACGCTTGAAGA 424
Db 377 GCGCACTGCTCGCTTCTGGGCTGCTACGCGGACGACAGTTGTTTCCAGCTGGTACG 436
Qy 425 GTGTTCTAGCACTGAAGATGATGAGGCAAAAGAGCTACACTTTGAGCAAGCGGAAGAAG 484
Db 437 GCATGGTGAAGGCCAGCGGAGGAGGAGGCGGAGAGCGGAAGCGAGACGCTCGCG 496
Qy 485 TGCTTGAGAGGTGCGAAGAGTGTCAACAGTGCAGTGAAGGAGCGCTATTTTCGGAG 544
Db 497 CCATCGAGCACATGGAAGTGACCTTCGCAAGTGTCTCGCGCGCAACGCCCTTCTCGGTG 556
Qy 545 GAGATACGATTGGATTGTTGACATTG 571
Db 557 CGGACTCATCGGCTACGTCACATCG 583
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## RESULT 15

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US-09-248-335-63
; Sequence 63, Application US/09248335
; Patent No. 6096504
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEF, DANIEL
; TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1128-A
; CURRENT APPLICATION NUMBER: US/09/248,335
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 08/924,759
; EARLIER FILING DATE: 1997-September-05
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 63
; LENGTH: 872
; TYPE: DNA
; ORGANISM: maize
US-09-248-335-63
```

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Query Match      14.2%; Score 130.8; DB 3; Length 872;
Best Local Similarity 49.1%; Pred. No. 4.8e-27;
Matches 403; Conservative 0; Mismatches 412; Indels 5; Gaps 2;

Qy 101 TGAGGCTTTTGGGTGCTTGGTTCACTTTCAGTCCATTGCGCCTGAGGCTGCAGATTGCCCTTAACC 160
Db 54 TGAAGCTGATCGGCGAGTACGGGAGCGGCTTCTGTAACGAGGCTTCTCTCAGCC 113
```

```
Qy 161 TCAGGGTTTGGATTATGAGTGTTCAGAGAGCTTTGAATCCCAAGTGAATTGCTTC 220
Db 114 TCAGGGGCTGAGCTACGAGTACGTCGAGGAGGATCTCAGAAAACAAGAGCGCGCTCTCTCC 173
Qy 221 TTAAGTCCAAACCCCTGTGCACAAAGAAAATCCAGATTTTCTTCCATGGAGATAAAGTCAAT 280
Db 174 TCAGCTCCAAACCCCGTGCACAAAGCGGTTCAGTGTGATCCACAGAGGCAAGCTATCT 233
Qy 281 GTGAATCTGCAATCATATAGTTGAGTACATAGATGAGGTTTGGTCCAAATGCTCTCTCCA 340
Db 234 GCGAGTCGAGGTTCATCGTCAGTACATCGACGAGGCTTTGCGCGCATCGCGCCGCC 293
Qy 341 TCCTTCCACAAAATGATATGATCGAGCTAATGCCGATTTTGGSTTTTCTTACATCGATG 400
Db 294 TCCTTCCCGCGCGACCCCTACGAAACGCTCGGTGGCCCGTTCTTGGGCTGCCTTCATTGAAG 353
Qy 401 ACAAGTGGCTTACGTCCTTGAAAAGTGTTCCTAGCGACTGAAAGATGATGAGGCAAGAAGC 460
Db 354 ACAAGCTTGTGTCCCCGTGGACCGAGTGTTCGGGCGAAGACGAGAGGAGGAG 413
Qy 461 TACACTTTGAGCAAGCGGAAGAGTGTCTGAGAAAGTGGAGAAAGTGTTCACAAAGTGCA 520
Db 414 AGGCGATGAAGCAGATGCTTTGCGGCGAGTGCACGCTCTGGAGGGAGCACTGAAGGAGGGA 473
Qy 521 GTGAAGGGAAGGCTATTTCCGAGGAGATAGGATTTGATTTGTTGACATTTGGTTTGGAA 580
Db 474 G---ACCCAGACCCCTTCTCGGCGGCGACACGCTCGGGTACGTGGACGTCGTTCTGGGCG 530
Qy 581 GCTTTTGTGAGTTTCATTTAGAGTCTCAGAGAATATGAATGAAAGAAAATTTGCTTCATGAAA 640
Db 531 GTGCCGTCTCGTACGCCAAGGGGACACGCGGCTCTTCGGTTCGAGCTCATCGACGCCG 590
Qy 641 CGAAGTACCTGTTGACCCCTATGGGCTGAAACTTTTGTGCTGATCTCTGCTGTGAAG 700
Db 591 CCAAGACCGCGCTCTCGCGCGCTGGATGGAGCGCTTCTGCGAGCTCGACCGCGCCAAAG 650
Qy 701 GCCTTCTGCCAGAGACTGAAAAGCTTGTGAGTTTGCAAAAGATTTCTTCAGCTAAATGGG 760
Db 651 CGGTCTTGCAGGAGCTGATAGAGTGTTCAGTACGGAAGATGCTGATCGCCCAAGATG 710
Qy 761 CTGCTGCAGCTGCTGCAAAAGTAAATGGAATCAAAATTAAT--TGCTGGATGAATTTCAAAA 818
Db 711 CTGCTGCACATCGTCAGGCGTAGTGTGTTTCTGATCGATCAGCTTGTATGTATGATTA 770
Qy 819 ATTGTTGTGCAAGTTATTTATATCTGAGGCTATGTTTGTGCAACTTTTATATATTTAAA 878
Db 771 GAACCTTGTAAAAACCAAAATCGTTCAAGTTTGATGTAAGTTCCATGTTAGAAAAA 830
Qy 879 GTCAAAATAAATGTTATGATAATATAGTAAAAA 918
Db 831 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 870
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Job time : 90 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 23:53:06 ; Search time 2946 Seconds

(without alignments)

9305.323 Million cell updates/sec

Title: US-10-088-945A-14

Perfect score: 918

Sequence: 1 cataaaactccacatttcct.....aatatagtaaaaaaaaaa 918

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST.\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
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13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592.2	64.5	614	14	CF922626 GmtrRw24
2	486.4	53.0	579	13	BU084645 Bar26a06
C 3	475.2	51.8	691	10	BE823032 GM700019B
C 4	461.6	50.3	604	14	CD406010 Gm_ck3016

5	461.2	50.2	614	10	AW471665
6	453.6	49.4	566	12	BG157232
7	439.4	47.9	601	13	BU764540
8	438	47.7	581	12	BI427624
C 9	436.8	47.6	458	10	AW349581
C 10	422	46.0	707	14	CD400374
11	414.2	45.1	553	13	BU091596
12	413.6	45.1	534	10	BG043636
13	413.4	45.0	601	10	AW760276
14	402	43.8	630	10	BE556267
15	382.8	41.7	502	12	BG653588
16	373.8	40.7	627	13	BQ140801
17	371.6	40.5	539	10	BG047474
18	370.4	40.3	372	9	AI440996
19	364.8	39.7	616	10	BF520786
20	356.4	38.6	489	10	AW734511
21	354.4	38.4	583	14	CA953253
22	352.8	38.4	597	10	BF519757
23	341.4	37.2	671	14	CB893410
24	329.8	35.9	606	10	BF639128
25	326.6	35.6	530	14	CA953342
26	322.8	35.2	500	13	BQ610460
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28	315.8	34.4	775	14	CA923160
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30	311.4	33.9	458	14	CD396596
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32	303.8	33.1	504	10	BF716119
33	297	32.4	841	14	CF510854
34	294.8	32.1	790	14	CF510677
35	291.4	31.7	456	10	BF068201
36	291	31.7	695	14	CF837076
37	289.8	31.6	401	10	BE801758
38	288.8	31.5	721	14	CF837075
39	280.2	30.5	721	14	CA411506
40	278.4	30.3	639	14	CD278180
41	278.2	30.3	666	14	CK111039
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#### ALIGNMENTS

RESULT 1

CF922626

LOCUS

DEFINITION

CF922626

VERSION

KEYWORDS

SOURCE

ORGANISM

CF922626

EST.

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 614)

Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

Expressed sequence tags from soybean root hair subtractive cDNA

library

Unpublished (2003)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-4752

Fax: 573-882-0588

Email: staceygm@missouri.edu

Single pass sequence

Seq primer: T7.

CF922626 614 bp mRNA linear EST 05-NOV-2003  
GmtrRw24-13-T7\_D07\_1\_057 Soybean root hair subtracted cDNA library  
GmtrRw24 Glycine max cDNA, mRNA sequence.

CF922626

CF922626.1

EST.

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 614)

Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

Expressed sequence tags from soybean root hair subtractive cDNA

library

Unpublished (2003)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-4752

Fax: 573-882-0588

Email: staceygm@missouri.edu

Single pass sequence

Seq primer: T7.

FEATURES	Location/Qualifiers	
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source	/organism="Glycine max"	
	/mol_type="mRNA"	
	/cultivar="Williams 82"	
	/db_xref="taxon:3847"	
	/tissue_type="root hairs"	
	/clone_lib="Soybean root hair subtracted cDNA library gmrhRw24"	
ORIGIN	/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Bradyrhizobium japonicum for 24 hours."	
	Query Match 64.5%; Score 592.2; DB 14; Length 614;	
	Best Local Similarity 99.3%; Pred. No. 1.1e-105;	
	Matches 605; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	
Qy	307	ATAGATGAGGTTTGTCACCAATGCTCTCTCCATCTTCCACAAATGCAATATGATCGA 366
Db	1	ATAGATGAGGTTTGTCCTCCATCTCTCCATCTTCCACAAATGCAATATGATCGA 59
Qy	367	GCTAATGCCCATTTGGGTTCTTACATGATGACAGTGGCTTACGTCCTTGAAAGT 426
Db	60	GCTAATGCCCATTTGGGTTCTTACATGATGACAGTGGCTTACGTCCTTGAAAGT 119
Qy	427	GTTCTAGCGACTGAAGATGATGAGCAAGAGCTACACTTTTGAGCAAGCGGAAGAGTG 486
Db	120	GTTCTAGCGACTGAAGATGATGAGCAAGAGCTACACTTTTGAGCAAGCGGAAGAGTG 179
Qy	487	CTTGAGAAAGTGGAGAGTGTTCACAAAGTGCAGTGAAGGAGGCGCTATTTCCGAGGA 546
Db	180	CTTGAGAAAGTGGAGAGTGTTCACAAAGTGCAGTGAAGGAGGCGCTATTTCCGAGGA 239
Qy	547	CATACGATTGATTTGTCGATTTGTTGCAAGCTTTTGGAGCTTTTTCAGTTTCATTAGAGTCTCA 606
Db	240	CATACGATTGATTTGTTGCAATTTGTTGGAAGCTTTTTCAGTTTCATTAGAGTCTCA 299
Qy	607	GAGTAATGAATGAAGAAATTTGCTGATCAAGCAAGTACCTTGGTTTCACCTATGG 666
Db	300	GAGTAATGAATGAAGAAATTTGCTGATGAAGCAAGTACCTTGGTTTCACCTATGG 359
Qy	667	GCTGAACTTTTGCTGCTGATCTCTGCTGTAAGGCGCTTCTGCCAGAGACTGAAAGCTT 726
Db	360	GCTGAACTTTTGCTGCTGATCTCTGCTGTAAGGCGCTTCTGCCAGAGACTGAAAGCTT 419
Qy	727	GTTGAGTTTGAAGATTTCTCAGTAAATGGGCTGCTGCAAGTAAATG 786
Db	420	GTTGAGTTTGAAGATTTCTCAGTAAATGGGCTGCTGCAAGTAAATG 479
Qy	787	GAATCAAAATTAATTGCTGATGAATTTCAAAAATTTGTTGCAAGTTATTTATATCTGAG 846
Db	480	GAATCAAAATTAATTGCTGATGAATTTCAAAAATTTGTTGCAAGTTATTTATATCTGAG 539
Qy	847	GCTATGTTTGTGCAACTTTATATATTTAAAGTCAAAATAAATTTATGATAATAGT 906
Db	540	GCTATGTTTGTGCAACTTTATATATTTAAAGTCAAAATAAATTTATGATAATAGT 599
Qy	907	AAAAAAAAA 915
Db	600	AAAAAAAAATA 608
RESULT 2		
BU084645		
LOCUS	BU084645 579 bp mRNA linear EST 27-AUG-2002	
DEFINITION	sar26a06.y1 Gm-cl049 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl049-7691 5', similar to TR:Q9SEK1 Q9SEK1 GLUTATHIONE S-TRANSFERASE 3 ;, mRNA sequence.	
ACCESSION	BU084645	
VERSION	BU084645.1 GI:22525834	
KEYWORDS	EST.	
SOURCE	Glycine max (soybean)	

ORGANISM	Glycine max	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	
REFERENCE	1 (bases 1 to 579)	
	Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.	
TITLE	Public Soybean EST Project	
	Unpublished (1999)	
JOURNAL	Contact: Shoemaker R/Public Soybean EST Project	
	Public Soybean EST Project	
COMMENT	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@watson.wustl.edu	
	This clone is available through: ResGen, Invitrogen Corp. 2130	
	South Memorial Parkway Huntsville, AL 35801 For further information	
	call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com	
FEATURES	Seq primer: -40RP from Gibco	
	High quality sequence stop: 421.	
source	Location/Qualifiers	
	1..579	
	/organism="Glycine max"	
	/mol_type="mRNA"	
	/db_xref="taxon:3847"	
	/clone="SOYBEAN CLONE ID: Gm-cl049-7691"	
	/tissue_type="whole seedlings of greenhouse grown plants"	
	/dev_stage="3 week old"	
	/lab_host="Gm10B"	
	/clone_lib="Gm-cl049"	
	/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."	
ORIGIN	Query Match 53.0%; Score 486.4; DB 13; Length 579;	
	Best Local Similarity 91.5%; Pred. No. 5.2e-85;	
	Matches 527; Conservative 0; Mismatches 46; Indels 3; Gaps 1;	
Qy	79	ACAGTGATGGCTGAAGGAGCTTGAGGCTTTTGGTGCTTGGTTCAGTCCATTGGCCTG 138
Db	1	ACAGTGATGGCTCAAGGGAGCTTGAGGCTTTTGGTGCTTGGTTCAGTCCATTGGCCTG 60
Qy	139	AGGGTGCAGATTGCCCTTAACCTCAAGGGTTTGATTTATGAGGTTGTTGAAGAGACTTTG 198
Db	61	AGGGTGCAGATTGCCCTTAACCTCAAGGGTTTGATTTATGAGGTTGTTGAAGAGACTTTG 120
Qy	199	AATCCCCAAAAGTGAATGCTTCTTAAGTCCAACTGTGCACAGAAAAATCCCAAGTTTTC 258
Db	121	AATCCCCAAAAGTGAATGCTTCTTAAGTCCAACTGTGCACAGAAAAATCCCAAGTTTTC 180
Qy	259	TTCCNTGGAGATAAGTCATATGTCGATCTGCAATCATAGTTGAGTACATAGTAGAGTT 318
Db	181	TTCCNTGGAGATAAGTCATATGTCGATCTGCAATCATAGTTGAGTACATAGTAGAGTT 240



```
RESULT 4
CD406010/c
LOCUS      CD406010      604 bp      mRNA      linear      EST 07-JUN-2003
DEFINITION Gm.ck30160 Soybean induced by Salicylic Acid Glycine max cDNA 3',
            mRNA sequence.
ACCESSION  CD406010
VERSION     CD406010.1  GI:31463982
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 604)
AUTHORS    Tian,A.-G., Wang,J., Cui,P., Han,Y.-J., Xu,H., Cong,L.-J.,
            Huang,X.-G., Wang,X.-L., Jiao,Y.-Z., Wang,B.-J., Wang,Y.-J.,
            Zhang,J.-S., Chen,S.-Y. and Yu,J.
TITLE       Soybean Expressed Sequence Tags Sequencing
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen S-Y
            Plant Biotechnology Laboratory
            Institute of Genetics and Developmental Biology, CAS, China
            Datun road, Beijing 100101, China
            Tel: 86-10-64886859
            Fax: 86-10-64873428
            Email: sychen@genetics.ac.cn
            Email: sychen@genetics.ac.cn
            Seq primer: T7 primer.
            Location/Qualifiers
                1..604
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Kefeng 1"
                /db_xref="taxon:3847"
                /tissue_type="Seedlings"
                /dev_stage="two-week seedlings"
                /lab_host="XLI-Blue MRF, strain"
                /clone_lib="Soybean induced by Salicylic Acid"
                /note="Vector: pBluescript SK+; Site_1: EcoR I; Site_2:
                Xho I; The cDNA library was constructed by He, C-Y from
                mRNA isolated from two-week seedlings (cultivar Kefeng 1)
                treated by spraying 2.0mM salicylic acid for 24, 36, 48
                and 72 h. Complementary DNA was synthesized from mRNA
                using a primer consisting of a poly(dT) sequence with a
                XhoI restriction site. EcoRI adapters were ligated to the
                blunt-ended cDNA fragments followed by XhoI digestion. The
                cDNA fragments were directionally cloned into the
                EcoRI-XhoI restriction site of the pBluescript vector. The
                ligated cDNA fragments were transformed into XLI-Blue MRF,
                host cells (Stratagene)."
```

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Db      427  AAGATGATGAGGCAAGAAAGCCACACTTTGAGCAAGCAGAAAGGCTTGAGAGGTGG 368
Qy      500  AAGAAGTGTTCACAACTGCAGTGAAGGAGGCTATTTTCGGAGGAGATACGATTGGAT 559
Db      367  AAGAAAGTGTTCACAACTGCAGTGAAGGAGGCTATTTTCGGAGGAGATACGATTGGAT 308
Qy      560  TTGTTGACATTTGGTTTGGAAAGCTTTTGGAGTTTCATTAGAGTCTCAGAGAATATGAATG 619
Db      307  TCATTGACATTTGGTTTGGGAGCTTCTTGAGTTGGATGAGAGTCATAGAGGAGATGAGTG 248
Qy      620  AAAGAAAATTGCTTGATGAACGAGTACCTGGTTTGACCCCTATGGCTGGAACCTTTTG 679
Db      247  GAAGAAAATTGCTTGATGAACGAGTACCTGGTTTGACCCCTATGGCTGGAACCTTTTG 188
Qy      680  CTGCTGATCTCTGCTGCAAGGGCTTCTGCGAGAGACTGAAAAGCTTGTGTGAGTTTGCAA 739
Db      187  CTGCTGATCTCTGCTGCAAGGGCTTCTTCCAGAGACTGATAGCTTGTGTGAGTTTGCCA 128
Qy      740  AGATTCTTCAGCTAAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Db      127  AGATTCTTCAGCTAAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 71
Qy      800  TGCTGGATGAATTCAAAATTTGTCGAAGTATTATATCTGAGGCTATGTTGCTGCTG 859
Db      70  TGGGAGA-GTATTTTCAAAATTTGTGTCAAGTGTGTTTATCTCAGGCTATG-TTGTG 13
Qy      860  CAACTTTATATA 871
Db      12  CAACTTTATATA 1
            |||||
            |||||

RESULT 5
AW471665
LOCUS      AW471665      614 bp      mRNA      linear      EST 03-DEC-2001
DEFINITION sl14cl1.y1 Gm-cl029 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            S-TRANSFERASE TSI-1 ; mRNA sequence.
ACCESSION  AW471665
VERSION     AW471665.1  GI:7041771
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 614)
AUTHORS    Shoemaker,R., Reim,P., Vodkin,L., Erpelding,J., Coryell,V.,
            Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
            Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
            Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
            Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
            Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            High quality sequence stop: 441.
            Location/Qualifiers
                1..614
                /organism="Glycine max"
                /mol_type="mRNA"
                /db_xref="taxon:3847"
                /clone="GENOME SYSTEMS CLONE ID: Gm-cl029-1197"
                /tissue_type="very young cotyledons of greenhouse grown"

FEATURES
            source
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Qy 397 GATGACAAAGTGGCTTACGTCCTTGAAGAGTGTCTTAGCGACTGAAGATGATGAGGCAAG 456  
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 Db 303 GATGAGAAGTGGTTTACGTCCTTGAAGAGTGTCTTAGTGGCTGAAGATGATGAGGCAAG 362  
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 Qy 457 AAGCTACACTTTGAGCAAGCGGAAGAGTGTCTGAGAAGGTGGAAGAGTGTTCACAAAG 516  
 |||||  
 Db 363 AAGCCACACTTTGAGCAAGCAAGAGAGGGCTTGAGAGGTGGAAGAGTGTTCACAAAG 422  
 |||||  
 Qy 517 TGCAGTGAAGGGAAGGCGCTATTTCGGAGGAGATACGATTGGATTGTGACATTGGTTTT 576  
 |||||  
 Db 423 TACAGTGAAGGGAAGGCGCTATTTCGGAGGAGATACGATTGGAATTCATTGACATTGGGTTT 482  
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 Qy 577 GGAAGCTTTTTCAGTTCATTAGAGTCTTCAGAGAAATATGAATGAAGAAAAATTCCTTGAT 636  
 |||||  
 Db 483 GGGAGCTTCTTGAAGTGGATGAGATCATAGAGAGATGAGTGGAGAAATTCCTTGAT 542  
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 Qy 637 GAAACGAAGTACCTCGTTTGACC 660  
 |||||  
 Db 543 TGAAGAAAGCACCTTGTGTTGGCC 566  
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RESULT 7  
 BU764540  
 LOCUS  
 DEFINITION  
 sas03a07.y2 Gm-cl080 Glycine max cDNA clone SOYBEAN CLONE ID:  
 Gm-cl080-2701 5', similar to TR:Q9SEK1 Q9SEK1 GLUTATHIONE  
 S-TRANSFERASE 3 ; mRNA sequence.

ACCESSION  
 BU764540  
 VERSION  
 BU764540.1 GI:23732736  
 KEYWORDS  
 EST.  
 SOURCE  
 Glycine max (soybean)  
 ORGANISM  
 Glycine max

REFERENCE  
 1 (bases 1 to 601)  
 Shoemaker,R., Keim,P., Vodkin,L., Erpelnding,J., Coryell,V.,  
 Khanna,A., Holla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
 Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
 Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,  
 Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact: ccu@resgen.com web site:  
 www.resgen.com

FEATURES  
 source  
 1. .601  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl080-2701"  
 /tissue\_type="Roots of 8 day old 'Bragg' supernodulating  
 mutant NTS382 seedlings"  
 /dev\_stage="8 days old"  
 /lab\_hosts="DH10B"  
 /clone\_lib="Gm-cl080"  
 /note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2:  
 XhoI; The mRNA was isolated from roots of 8 day old  
 'Bragg' supernodulating mutant NTS382 seedlings that were

infected with *Bradyrhizobium japonicum*, strain USDA 110, 72  
 hours prior to harvest. Dr. Gary Stacey generously donated  
 the tissue. The roots were flash-frozen in liquid  
 nitrogen. Stratagene's cDNA Synthesis Kit (catalog number  
 204001) was used to synthesize the cDNA. First-strand  
 synthesis was performed with 5-methyl dCTP, hence the  
 ligated cDNA was hemimethylated. A modification of  
 Stratagene's first-strand synthesis primer was used. An  
 'anchor' nucleotide (V=A, C, or G) was added to the 3' end  
 of the primer [GAGAGAGAGAGAGAGAACTAGTCGAG(T)18V] to  
 anchor the primer at the 5' end of the poly(A) tract.  
 After second-strand synthesis, the cDNA ends were filled  
 in with cloned Pfu DNA, ligated to EcoRI adapters and  
 subsequently phosphorylated. The cDNA was then  
 precipitated and redissolved in sterile, RNase-,  
 DNase-free water. The XhoI site within the first- strand  
 synthesis primer was then restricted by digestion with  
 XhoI from Promega (400/ul); all XhoI sites in the cDNA  
 would be protected by their hemimethylated status. The  
 cDNA constructs were size-fractionated with a 500bp  
 cutoff, using Sephacryl S-500 High Resolution (Pharmacia  
 Biotech) in a 2-mm diameter column and a bed volume of  
 approximately 1ml. The column eluent was precipitated,  
 redissolved, and ligated into Stratagene's pBluescript II  
 XR Predigested vector (pBluescript II SK(+)) vector that  
 has been digested with EcoRI and XhoI, and phosphorylated  
 by Stratagene). This library was constructed in the  
 laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at  
 Northern Arizona University."

## ORIGIN

Query Match 47.9%; Score 439.4; DB 13; Length 601;  
 Best Local Similarity 85.2%; Pred. No. 7.7e-76;  
 Matches 507; Conservative 0; Mismatches 76; Indels 12; Gaps 1;

Qy 75 GTAAACAGTATGGCTGAAGGACTTGGGCTTTGGGTGCTTGGTTCAGTCCATTGC 134  
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 Db 1 GTGAATAGAAATGGCTAAAAACGAGTTGAGGCTTTTGGGTGCTTGGTTCATATGC 60  
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Qy 135 CCTGAGGCTGCAGATTGCCCTTAACCTCAAGGGTTTGGATTATGAGGTGCTTGAAGAGAC 194  
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Qy 195 TTTGAATCCCAAAAGTGAATTGCTTCTTAAGTCAACCCCTGTGCACAAGAAAATCCCACT 254  
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 Db 121 CTTGAATCCCAAAAGTGAATTGCTTCTTAAGTCAACCCCTGTGCACAAGAAAATCCCACT 180  
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Qy 255 TTTCTTCATGGAGATAAAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGA 314  
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 Db 181 TCTACTCCATGGATATTAAATTCAATGTGAATCTGCAATCATAGTAGATACATAGATGA 240  
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Qy 315 GGTTCGTGCAACAATGCTCTCTCCATCCTTCCACAATAATGCATATCATGAGCTAATGC 374  
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 Db 241 GGTTCGTGCAACAATGCTCTCTCCATCCTTCCACAATAATGCATATGAGCTAATGC 300  
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Qy 375 CCGATTTTGGGTTCTTTACATCGATGACAAGTGGCTTACGTCCTTGGAAAAGTGTCTTAGC 434  
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 Db 301 CCGATTTTGGGTTCTTTACATCGATGACAAGTGGTATACGTCCTCATAGGAATACTATTT 360  
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Qy 435 GACTG-----AAGATGATGAGGCAAGAAGACTACACTTTGAGCAAGCGGAAGA 482  
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 Db 361 GGCTGAAGCGGCTGATCAAGATGATGAGGCAAGAAGCCACACTTGTGAGAATGGAAGA 420  
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Qy 483 AGTGCTTGAGAAGGTGGAAGAAGTGTTCACAAGTGCAGTGAAGGGAAGGCTATTTTCGG 542  
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 Db 421 AGCTTTTGAGAGGATGGAAGAAGTGTTCACAAGTGCAGTGAAGGGAAGGCTTATTTGG 480  
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Qy 543 AGGAGATACGATTGGATTGTTGACATTGGTTTTTGGAAAGCTTTTGTAGATTTCATTAGAT 602  
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 Db 481 AGGAGATACATTGGAATTATTGACATTGCTTTTGGGAGCCTTTGGGGTGGGTGAGAT 540  
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Qy 603 CTCAGAGATATGAATGAAGAAGAAATTCCTTGATGAACGAAGTACCCCTGTTTG 657  
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/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="Gm-r1021-1790"
/tissue_type="root"
/lab_host="XL10-Gold"
/clone_lib="Gm-r1021"
/note="vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Library Gm-r1021 is a sequence-driven, rerecked set
of the original library Gm-cl004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. StrataGene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize
the cDNA. The Gm-cl004 library was constructed by Dr.
Paul Keim & Virginia H. Coryell, Department of Biology,
Box5640, Northern Arizona University, Flagstaff, AZ
86011, email: paul.keim@uau.edu, virginia.coryell@uau.edu.
The contig analysis to select unique genes was performed
by the laboratory of Ernest Retzel, Computational Biology
Centers, University of Minnesota,
http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
. Reracking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and sequencing by the Keck
Center for Comparative and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."

```

## ORIGIN

```

Query Match      47.6%; Score 436.8; DB 10; Length 458;
Best Local Similarity 97.4%; Pred. No. 2.6e-75;
Matches 444; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 418 TTGAAAGTGTCTAGCGACTGAAGATGATCAGCGCAAGAGCTACACTTTTGACAGCG 477
Db 456 TTGAAAGTGTCTAGCGACTGAAGATGATCAGCGCAAGAGCTACACTTTTGACAGCG 397

Qy 478 GAAGAAGTGTCTGAGAAGGTGGAAGAGTGTTCACCAAGTGCAGTGAAGGGAAGCCCTAT 537
Db 396 GAAGAAGTGTCTGAGAAGGTGGAAGAGTGTTCACCAAGTGCAGTGAAGGGAAGCCCTAT 337

Qy 538 TTCGAGGAGATACGATTGGATTTGTGACATTTGGTTTGGAACTTTTGGAGTTTCATT 597
Db 336 TTCGAGGAGATACGATTGGATTTGTGACATTTGGTTTGGAACTTTTGGAGTTTCATT 277

Qy 598 AGAGTCTCAGAGATATCAATGAAGAAATTTGCTGATGAAGCAAGTACCCCTGGTTTG 657
Db 276 AGAGTCTCAGAGATATCAATGAAGAAATTTGCTGATGAAGCAAGTACCCCTGGTTTG 217

Qy 658 ACCCTATGGGCTGAAACTTTTGTGCTGATCCTCTGTGAGGGCCCTTCTGCCAGAGACT 717
Db 216 CCCCTATGGGCTGAAACTTTTGTGCTGATCCTCTGTGAGGGCCCTTCTGCCAGAGACT 157

Qy 718 GAAAGCTTGTGAGTTTGAAAGATTTCTCAGCTAAATGGGCTGCTGCAGCTGCTGCA 777
Db 156 GAAAGCTGTTGAGTTTAGCAAGATTTCTCAGTTAAATGGGCTGCTGCAGCTGCTGCA 97

Qy 778 AAGTAAATGGAATCAAAATTAATTCGTGATCAATTTCAAAATTTGTTGCAAGTTATT 837
Db 96 AAGTAAATGGAATCAAAATTAATTCGTGATCAATTTCAAAATTTGTTGCAAGTTATT 37

Qy 838 ATATCTGAGGCTATGTTTGTGTTGCAACTTTTATATATT 873
Db 36 ATATCAGAGGCAATGCTGTTGCACTTTATATATT 1

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## RESULT 10

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CD400374/c
LOCUS      Gm_ck22228 Soybean induced by Salicylic Acid Glycine max cDNA 3',
DEFINITION mRNA sequence.
ACCESSION CD400374
VERSION   CD400374.1 GI:31458346

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## KEYWORDS

SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

## REFERENCE

1 (bases 1 to 707)

Tian,A.-G., Wang,X.-J., Cui,P., Han,Y.-J., Xu,H., Cong,L.-J.,  
Huang,X.-G., Wang,X.-L., Jiao,Y.-Z., Wang,B.-J., Wang,Y.-J.,  
Zhang,J.-S., Chen,S.-Y. and Yu,J.  
Soybean Expressed Sequence Tags Sequencing  
Unpublished (2003)

## TITLE

Contact: Chen S-Y

## JOURNAL

COMMENT

Plant Biotechnology Laboratory  
Institute of Genetics and Developmental Biology, CAS, China  
Datun road, Beijing 100101, China  
Tel: 86-10-6486859  
Fax: 86-10-64873428  
Email: sychen@genetics.ac.cn  
Email: sychen@genetics.ac.cn  
Seq primer: T7 primer.

## FEATURES

Location/Qualifiers

source

1..707

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Kefeng 1"

/db\_xref="taxon:3847"

/tissue\_type="Seedlings"

/dev\_stage="two-week seedlings"

/lab\_host="XLI-Blue MRF strain"

/clone\_lib="Soybean induced by Salicylic Acid"

/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:

Xho I; The cDNA library was constructed by He, C-Y from

mRNA isolated from two-week seedlings (cultivar Kefeng 1)

treated by spraying 2.0mM salicylic acid for 24, 36, 48

and 72 h. Complementary DNA was synthesized from mRNA

using a primer consisting of a poly(dT) sequence with a

XhoI restriction site. EcoRI adapters were ligated to the

blunt-ended cDNA fragments followed by XhoI digestion. The

cDNA fragments were directionally cloned into the

EcoRI-XhoI restriction site of the pBluescript vector. The

ligated cDNA fragments were transformed into XLI-Blue MRF

host cells (Stratagene)."

## ORIGIN

```

Query Match      46.0%; Score 422; DB 14; Length 707;
Best Local Similarity 79.8%; Pred. No. 1.9e-72;
Matches 544; Conservative 0; Mismatches 115; Indels 23; Gaps 3;

Qy 209 GTGAATTGCTTCTTAAGTCCAAACCCCTGTGCACAAAGAAATCCCAAGTTTCTTCATGGAG 268
Db 707 GTGATCTGCTTCTTAAGTCCAAACCCCTGTGCACAAAGAAATCCCAAGTTTCTTCATGGAG 648

Qy 269 ATAAAGTCATATGTAATTCGCAATCATAGTTGAGTACATAGATGAGTTTGTGTCACAA 328
Db 647 ATAAAGTCATATGTAATTCGCAATCATAGTAGAGTACATAGATGAGTTTGTGTCACAA 588

Qy 329 ATGCTCTCTCCATCCCTTCCACAAATGCATATGATCGAGCTAATGCCGATTTTGGTTT 388
Db 587 ATGCTCTCTCCATCCCTTCCACAAATGCATATGATCGAGCTAATGCCGATTTTGGTTT 528

Qy 389 CTTTACATCGATGACAAAGTGGCTTACGTCCTTTGAAAAGTGTCTTAGCGACTG----- 439
Db 527 CTTTACATCGATGACAAAGTGGTATACGTCCTCAATAGGAATACTATTTTGGCTGAAGCGCTG 468

Qy 440 ---AAGATGATGAGGCAAGAAAGCTACATTTTGAGCAAGCGGAAGAGTGTCTTTGAGAGG 496
Db 467 ATCAAGATGATGAGGCAAGAAAGCCACACTTTGTGGAAATGGAAGAAGCTCTTTGAGAGGA 408

Qy 497 TGAAGAAGTGTTCACAAAGTCAGTCAGTGAAGGAGGCTATTTTCGGAGGAGATACGATTG 556
Db 407 TGAAGAAGTGTTCACAAAGTCAGTCAGTGAAGGAGGCTATTTTGGAGGAGATACAAATTG 348

```



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 534)

Shoemaker,R., Keim,P., Vodkin,L., Erpelnding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
Public Soybean EST Project

TITLE  
JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 994 Std Error: 0.00

High quality sequence stop: 424.

FEATURES

source

1..534  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl057-2021"  
/tissue type="Degenerating cotyledons, 2 week old seedling"  
/lab\_hosts="DH10B"  
/clone\_lib="Gm-cl057"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 45.1%; Score 413.6; DB 10; Length 534;  
Best Local Similarity 87.6%; Pred. No. 8.6e-71;  
Matches 468; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 67 CTGTTATAGTAAACAGTGAATGGCTGAAGGAGCTTGGGCTTTGGGTGCTTGGTTCAGT 126  
Db 1 CTGATATAGTCAATAGAAATGGCTAAAAACAGTTGAGGCTTTGGGTGCTTGGTTCAGT 60  
Qy 127 CCATTGGCCCTGAGGGTGCAGATTGCCCTTAACCTCAAGGCTTTGGATATAGAGTTGTT 186  
Db 61 CCATATGCCCTGAGGGTGCAGATTGCCCTTAACCTCAAGGCTTAGATATAGAGTTGTT 120  
Qy 187 GAAGAGACTTTGAATCCCAAAAGTGAATTGCTTCTTAAGTCCAAACCCCTGTGCACAAAGAA 246  
Db 121 GAAGAGACTTTGAATCCCAAAAGTGAATGCTGTTCTTAAGTCCAAACCCCTGTGCACAAAGAA 180  
Qy 247 ATCCAGTTTCTTCCATGGAGATAAAGTCATATGTGAATCGCAATCATAGTTGAGTAC 306  
Db 181 ATCCAGTTTCTTCCATGGAGATAAAGTCATATGTGAATCGCAATCATAGTTGAGTAC 240  
Qy 307 ATAGATGAGGTTTGGTCCAAACAAAGCTCTCTCCATCCTTCCACAAATGCATATGATCGA 366  
Db 241 ATAGATGAGGTTTGGTCCAAACAAAGCTCTCTCCATCCTTCCACAAATGCATATGATCGCA 300

Qy 367 GCTAATGCCGATTTTGGGTTTCTTACATCATGACAAAGTGGCTTACGTCTTGAAAAAGT 426  
Db 301 GCTAATGCCGATTTTGGGTTTCTTACATCATGACAAAGTGGTATACGTCCATAAGGAAT 360  
Qy 427 GTTCTAGCGACTG-----RAGATGATGAGCGAAGAGCTACACTTTTGACCAA 474  
Db 361 ACTATTTTGGCTGAAGCGGCTGATCAAGATGATGAGGCAAAAGACCCACACTTTTGTGGGA 420  
Qy 475 GCGGAAGAAGTGTCTTGAGAAGGTGGAAAGAGTGTTCACAAAGTGCAGTGAAGGGAAGGCC 534  
Db 421 ATGGAAGAACTCTTGTAGAGATGGAAGAGTGTTCACAAAGTGCAGTGAAGGAGGGCT 480  
Qy 535 TATTTCGAGGAGATACGATTGGATTGTTGACATTGGTTTGGAGCTTTTGG 588  
Db 481 TATTTTGGAGGAGATACAAATTGGAATTATTGACATTGCTTTTGGAGCCTTTTG 534

RESULT 13

AW760276

LOCUS

DEFINITION

AW760276 601 bp mRNA linear EST 03-DEC-2001  
sl48c04.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl027-4543 5' similar to TR:004562 O04562 T7N9.15. ;, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelnding,J., Coryell,V.,

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,

Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,

Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,

Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,

McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 1392 Std Error: 0.00

High quality sequence stop: 425.

FEATURES

source

1..601  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-4543"  
/tissue type="cotyledons of 3- and 7-day-old Williams seedlings"

/lab host="DH10B"

/clone\_lib="Gm-cl027"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; This cDNA library was constructed from mRNA isolated

from cotyledons of 3- and 7-day-old Williams seedlings

which were propagated on paper towels with distilled

water. The cotyledons were flash-frozen in liquid

nitrogen, then lyophilized for 72 hours. Unequal amounts

of mRNA was used for cDNA synthesis. Stratagene's cDNA

Synthesix Kit (catalog number 200401) was used to

synthesize the cDNA. First- stranded synthesis was

performed with 5-methyl dCTP, hence the ligated cDNA was





Db 247 GAGTACATAGATGAGTTGGTCCCAACAATGCTCTCTCCATCCTTCCACAAAATGCTTAT 306  
 QY 361 GATCAGAGTAATGCCCGATTTGGTCTTTTACATCGATGACAAAGTGCTTACGTCCTTG 420  
 Db 307 GACCCAGCTAATGCCCGATTTGGGTTTCTTACATCGATGACAAAGTGCTATACGTCACATA 366  
 QY 421 AAAAGTGTTTACGACATG-----AAGATGATGAGGCAAGAAGCTACACTTT 468  
 Db 367 AGGAATACTATTTTGGCTGGAAGCGCTGATCAAGATGATGAGGCAAGAAGCTACACTTT 426  
 QY 469 GAGCAAGCGGGAAGAGTCTTGAAGAGTGAAGAAGTGTTCACAAAGTGCAAGTGAAGGG 528  
 Db 427 GTGAGATGGAAGAAGCTCTTGAGAGGATGAAGAAGTGTTCACAAAGTGCAAGTGAAGGA 486  
 QY 529 AAGGCTATTTCGGAGGAGATACGATTTGGATTTTGTGACATTTGGTTTTTGGAGGCTTTT 588  
 Db 487 AGGGCTATTTTGGAGGAGATCAATTGGA-TTATTGACATTTGTTTGGAGGCTTTGGG 545  
 QY 589 AGTT 592  
 Db 546 GGTT 549

## RESULT 15

BG653588

LOCUS

DEFINITION BG653588.1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE  
 ID: Gm-cl051-6257 5', similar to TR:Q9XIF8 Q9XIF8 F23H11.1 PROTEIN.  
 ; mRNA sequence.

ACCESSION BG653588

VERSION BG653588.1 GI:13790997

KEYWORDS

SOURCE Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

## REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Expelding,J., Coryell,V.,  
 Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
 Beck,C., Wylie,I., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
 Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,  
 Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.  
 Public Soybean EST Project  
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130  
 South Memorial Parkway Huntsville, AL 35801 For further information  
 call: (800)-533-4363 or contact via email: ccu@resgen.com  
 High quality sequence stop: 416.

## FEATURES

source

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 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl051-6257"  
 /tissue\_type="floral meristematic mRNA"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl051"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; The cDNA library was constructed from floral  
 meristematic mRNA provided by Dr. Halina Knap of Clemson  
 University. Complementary DNA was synthesized from mRNA  
 using a primer consisting of a poly(dT) sequence with a  
 XhoI restriction site. EcoRI adapters were ligated to the

blunt-ended cDNA fragments followed by XhoI digestion. The  
 cDNA fragments were directionally cloned into the  
 EcoRI-XhoI restriction site of the pBluescript vector. The  
 ligated cDNA fragments were transformed into DH10B host  
 cells (GibcoBRL). This library was constructed in the  
 laboratory of Dr. Randy Shoemaker."

## ORIGIN

Query Match 41.7%; Score 382.8; DB 12; Length 502;  
 Best Local Similarity 87.2%; Pred. No. 9e-65;  
 Matches 436; Conservative 0; Mismatches 52; Indels 12; Gaps 1;  
 QY 115 GCTTGGTTAGTCATTTGCCCTGAGGTCACAGTTGCCCTTAACCTCAAGGGTTTGAT 174  
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 QY 175 TATGAGGTTGTTGAAGAGACTTTTGAATCCCAAAAGTGAATTTGCTTTAAAGTCCAAACCT 234  
 Db 62 TATGAGGTTGTTGAAGAGACCTTGAATCCCAAAAGTGAATTTGCTTTAAAGTCCAAACCT 121  
 QY 235 GTGCACAAAGAAAATCCCAAGTTTCTTCCATGGAGATAAAAGTCATATGTGAATCTGCAATC 294  
 Db 122 GTGCACAAAGAAAATCCCAAGTTTCTTCCATGGAGATAAAAGTCATATGTGAATCTGCAATC 181  
 QY 295 ATAGTTGAGTACATAGATGAGGTTTGGTCCAAACAATGCTCTCTCCATCTTCCACAAAAT 354  
 Db 182 ATAGTTGAGTACATAGATGAGGTTTGGTCCAAACAATGCTCTCTCCATCTTCCACAAAAT 241  
 QY 355 GCATATGATCGAGCTAATGCCGATTTTGGGTTTCTTACATCGATGACAAAGTGGCTTACG 414  
 Db 242 GCTTATGACCGAGCTAATGCCGATTTTGGGTTTCTTACATCGATGACAAAGTGGTATACG 301  
 QY 415 TCCTTGAAAAAGTGTCTTAGCGACTG-----AAGATGATGAGGCAAGAAGCTA 462  
 Db 302 TCCATAAGGAATACTATTTTGGCTGAAGCGGCTGATCAAGATGATGAGGCAAGAAGGCCA 361  
 QY 463 CACTTTGAGCAACGGGAAGAGTGTGAGAAAGTGTGAGAAAGTGTGTTCAACAAGTGCGAGT 522  
 Db 362 CACTTTGTGGGAATGGAAGAAGCTCTTGAGAGGATGGAAGAGTGTGTTCAACAAGTGCGAGT 421  
 QY 523 GAAGGGAAGGCTATTTCGGAGGAGATACGATTGGATTGTTGCATTTGGTTTGGGAAGC 582  
 Db 422 GAAGGGAAGGCTATTTCGGAGGAGATACAAATTGGAATTATTGACATTGCTTTTGGGAGC 481  
 QY 583 TTTTGGAGTTTTCATTAGAGT 602  
 Db 482 CTTTGGGTTGGTGAGAGT 501

Search completed: October 13, 2004, 05:50:02

Job time : 2952 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2004, 05:00:46 ; Search time 534 Seconds

(without alignments)  
8715.098 Million cell updates/sec

Title: US-10-088-945A-14

Perfect score: 918

Sequence: 1 cataaaactccacatttcct.....aatatagtaaaaaaaaaa 918

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues.

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887	96.6	1050	13	US-10-424-599-51507
2	623.2	67.9	1265	13	US-10-424-599-57938
3	288	31.4	896	9	US-09-765-213A-5
4	270	29.4	998	9	US-09-765-213A-1
5	268.4	29.2	947	9	US-09-765-213A-3
6	249.2	27.1	671	17	US-10-021-323-17539
7	240	26.1	684	9	US-09-938-842A-2676
8	240	26.1	684	11	US-09-938-842A-2676
9	232.2	25.3	705	9	US-09-938-842A-2658
10	232.2	25.3	705	11	US-09-938-842A-2658
c 11	228.2	24.9	817	9	US-09-770-445-743
c 12	222.8	24.3	779	16	US-10-260-238-4937
13	220	24.0	624	17	US-10-021-323-8555
14	212.4	23.1	606	17	US-10-021-323-499

15	206.6	22.5	589	17	US-10-021-323-15323	Sequence 15323, A
16	202.2	22.0	566	17	US-10-021-323-14067	Sequence 14067, A
17	201.2	21.9	552	17	US-10-021-323-14839	Sequence 14839, A
18	193.6	21.1	513	9	US-09-938-842A-1665	Sequence 1665, Ap
19	193.6	21.1	513	11	US-09-938-842A-1665	Sequence 1665, Ap
c 20	185.2	20.2	578	17	US-10-021-323-17631	Sequence 17631, A
21	181.8	19.8	684	9	US-09-938-842A-695	Sequence 695, App
22	181.8	19.8	684	11	US-09-938-842A-695	Sequence 717, App
c 23	181.4	19.8	824	9	US-09-770-445-717	Sequence 50534, A
24	181.2	19.7	971	17	US-10-437-963-50534	Sequence 52368, A
25	177.4	19.3	1128	17	US-10-437-963-52368	Sequence 45335, A
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27	172	18.7	743	17	US-10-767-701-7710	Sequence 48754, A
28	171	18.6	1121	17	US-10-437-963-48754	Sequence 13883, A
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30	169	18.4	980	13	US-10-425-114-5225	Sequence 28110, A
31	167.4	18.2	1067	13	US-10-425-114-28110	Sequence 19959, A
32	165	18.0	809	13	US-10-425-114-19959	Sequence 76241, A
33	163.8	17.8	333	13	US-10-424-599-76241	Sequence 45541, A
34	162.2	17.7	994	17	US-10-437-963-45541	Sequence 29311, A
35	161.2	17.6	921	17	US-10-437-963-29311	Sequence 84306, A
36	161.2	17.6	1004	17	US-10-437-963-84306	Sequence 13431, A
37	159.6	17.4	513	17	US-10-021-323-13431	Sequence 24808, A
38	157.6	17.2	851	13	US-10-425-114-24808	Sequence 22273, A
39	154.4	16.8	903	13	US-10-425-114-22273	Sequence 6569, Ap
40	154.2	16.8	998	17	US-10-437-963-6569	Sequence 26127, A
41	153.8	16.8	910	13	US-10-425-114-26127	Sequence 13603, A
42	153.8	16.8	1028	17	US-10-767-701-13603	Sequence 16335, A
c 43	153.6	16.7	516	17	US-10-021-323-16335	Sequence 4127, Ap
44	153.6	16.7	708	17	US-10-437-963-4127	Sequence 41800, A
45	151.4	16.5	1146	17	US-10-437-963-41800	

#### ALIGNMENTS

#### RESULT 1

US-10-424-599-51507  
; Sequence 51507, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 51507  
; LENGTH: 1050  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_17524C.1  
; US-10-424-599-51507

Query Match	96.6%	Score 887;	DB 13;	Length 1050;
Best Local Similarity	98.7%	Pred. No. 1.1e-220;		
Matches	905;	Conservative	0;	Mismatches 10;
		Indels	2;	Gaps 1;
Qy	1	CATAAAACTCCACATTTCTGCTGAGTAACCTTAACAAACAAACAAATATTTGCTCGTG	60	
Db	128	CATAAAACTCCACATTTCTGCTGAGTAACCTTAACAAACAAACAAACAGCATTTGCTCGTG	187	
Qy	61	TTTACCTGTTATAGTAACAGTATGCTGCTGAGGAGCTTTGAGGCTTTTGGGCTTGG	120	
Db	188	TTTACCTGTTATAGTAACAGTATGCTGCTGAGGAGCTTTGAGGCTTTTGGGCTTGG	247	
Qy	121	TTACGTCCATTTGGCCCTGAGGGTGCAGATTCCCTTAACCTCAAGGGTTTGGATTATGAG	180	

Db 248 TTCAGTCCATTTGTCCTGAGGGTCAGATGTCCTTAACTCAAGGGTTGGATTATGAG 307  
Qy GTTGTGAGAGACTTTGAATCCCAAAAGTGAATGCTTCTTAAGTCCAAACCCCTGTGCAC 240  
Db GTTGTGAGAGACTTTGAATCCCAAAAGTGAATGCTTCTTAAGTCCAAACCCCTGTGCAC 367  
Qy 241 AAGAAATCCAGTTTCTTCATGGAGATAAAGTCATATGATGTAATCTGCAATCATAGTT 300  
Db AAGAAATCCAGTTTCTTCATGGAGATAAAGTCATATGATGTAATCTGCAATCATAGTT 427  
Qy 301 GAGTACATAGATGAGTTTGGTCCCAAACTGCTCTCTCCATCTTCCCAAAATGCAATAT 360  
Db GAGTACATAGATGAGTTTGGTCCCAAACTGCTCTCTCCATCTTCCCAAAATGCAATAT 487  
Qy 361 GATCAGACTAATGCCCGATTTTGGTTCCTTACATCGATGACAAAGTGGCTTACGTCCTTG 420  
Db GATGAGCTAATGCCCGATTTTGGTTCCTTACATCGATGACAAAGTGGCTTACGTCCTTG 547  
Qy 421 AAAAGTGTTCAGCGACTGAA--GATGATGAGGCAAAAGACTACACTTTGAGCAAGCGG 478  
Db AAAAGTGTTCAGCGACTGAA--GATGATGAGGCAAAAGACTACACTTTGAGCAAGCGG 607  
Qy 479 AAGAGTGTTCAGAGGTGAGAGAGTGTTCACAAAGTGCAGTGAAGGGAGGCTTATT 538  
Db AAGAGTGTTCAGAGGTGAGAGAGTGTTCACAAAGTGCAGTGAAGGGAGGCTTATT 667  
Qy 539 TCGGAGGAGATACGATTTGATTTGTCACATGTTGTTGGAGGCTTTTGGAGTTTCATTA 598  
Db TCGGAGGAGATACGATTTGATTTGTCACATGTTGTTGGAGGCTTTTGGAGTTTCATTA 727  
Qy 599 GAGTCTCAGAGATATGAAATGAAAGAAATTTGCTTGATGAAACGAAGTACCTGGTTGA 658  
Db GAGTCTCAGAGATATGAAATGAAAGAAATTTGCTTGATGAAACGAAGTACCTGGTTGA 787  
Qy 659 CCCTATGGGCTGAAACTTTTCTGCTGATCTGCTGATGAGAGGGCTTCTGCCAGAGCTG 718  
Db CCCTATGGGCTGAAACTTTTCTGCTGATCTGCTGATGAGAGGGCTTCTGCCAGAGCTG 847  
Qy 719 AAAAGCTTTGTTGAGTTTCAAGATTTCTTCAAGTAAATGGGCTGCTGAGCTCTGCAA 778  
Db AAAAGCTTTGTTGAGTTTCAAGATTTCTTCAAGTAAATGGGCTGCTGAGCTCTGCAA 907  
Qy 779 AGTAAATGGAATCAAAATTAATGCTGGATGAATTTCAAAATTTGTTGCAAGTTATTTA 838  
Db AGTAAATGGAATCAAAATTAATGCTGGATGAATTTCAAAATTTGTTGCAAGTTATTTA 967  
Qy 839 TATCTGAGGCTATGTTGTTGCAACTTTATATATTTAAAGTCAAAATGATTTATGAT 898  
Db TATCTGAGGCTATGTTGTTGCAACTTTATATATTTAAAGTCAAAATGATTTATGAT 1027  
Qy 899 AATATAGTAAAAAATA 915  
Db AATATAGTAAAAAATA 1044

RESULT 2  
US-10-424-599-57938  
; Sequence 57938, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 57938  
; LENGTH: 1265  
; TYPE: DNA

; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_2332C.1  
US-10-424-599-57938  
Query Match 67.9%; Score 623.2; DB 13; Length 1265;  
Best Local Similarity 85.2%; Pred. No. 8e-152;  
Matches 758; Conservative 0; Mismatches 118; Indels 14; Gaps 5;  
Qy 30 CCTAACAAACAAACAAATATTGCTCCGTTTGTACCTCTGTATAGTAAACAGTATGGC 89  
Db 46 CCCAACAAAGCAACAACTTTGCCCTTGTAAACACTTCTTATTGTGATGCTTAAAG 105  
Qy 90 TGAAGGAGCTTGAAGGCTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGGTGCAGAT 149  
Db 106 CGAA--GACTTGAAGCTTTGGGAGGCTGGTTCAGCCCATTTGCCCTGAGGGTGCAGAT 162  
Qy 150 TGGCTTTAACTCAAGGGTTTGGATTAATGAGTTTGTGAAGAGACTTTTGAATCCCAAAAG 209  
Db 163 TGGCTTTAACTCAAGGGTCTAGAAATATGAGTTTGTGAAGAGACCTTGAATCCCAAAAG 222  
Qy 210 TGAATTCGCTTCTTAAGTCCAACTGTGCACAAAGAAATCCAGTTCCTTCCATGAGA 269  
Db 223 TGACCTGCTTCTTAAGTCCAACTGTGCACAAAGAAATCCAGTTCCTTCCATGAGA 282  
Qy 270 TAAAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGTTTGGTCCAAAC 329  
Db 283 TAAAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGGCTTGG--ACTAA 339  
Qy 330 TGCTCTCCATCTTCCCAAAATATGATATGATTCGAGCTTAATGCCCGATTTTGGGTTTC 389  
Db 340 TGTTCCTCCATCTTCCCAAAATATGATATGATTCGAGCTTAATGCCCGATTTTGGGTTTC 399  
Qy 390 TTACATCGATGACAAGTGGCTTACGCTTGAAGAGTGTCTAGCGACTCAAGATGATGA 449  
Db 400 CTACATTTGATGAGAAGTGGTTTACGCTTGTGAGAAGTGTCTAGTGGCTGAAGATGAGA 459  
Qy 450 GGCAAAGAAGCTACACTTTTGCAGCAAGCGGAAGTGTCTTGAAGAAGTGAAGAAGTGT 509  
Db 460 GGCAAAGAAGCTACACTTTTGCAGCAAGCGGAAGTGTCTTGAAGAAGTGAAGAAGTGT 519  
Qy 510 CAACAAGTGCAGTGAAGGAGGCTTATTTTCGAGGAGATACGATTCGATTTGTTGACAT 569  
Db 520 CAACAAGTGCAGTGAAGGAGGCTTATTTTCGAGGAGATAGCATTTGATTTGATTCAT 579  
Qy 570 TGGTTTGGAGGCTTTTGGAGTTTCAATGAGTCTCAGAGATATGATGAAAGAAAT 629  
Db 580 TGGTTTGGAGGCTTTTGGAGTTTGGATGAGATCATAGAGGATGATGAGGAGAAAT 639  
Qy 630 GCTTGATGAAACGAAGTACCTTGGTTTACCTTACCTTGGGCTGAAACCTTTTGTCTGATCC 689  
Db 640 GCTTGATGAAACGAAGTACCTTGGTTTACCTTGGGCTGAAACCTTTTGTCTGATCC 699  
Qy 690 TGTCTGAAGGGCTTCTGCCAGAGACTGAAAGCTTTGTTGAGTTTGCAGAGATTTCTTCA 749  
Db 700 TGTCTGAAGGGCTTCTTCCAGAGACTGATAAGCTTTGTTGAGTTTGCAGAGATTTCTTCA 759  
Qy 750 GCTAAATGCGCTGCTGCA-----GCTGCTGCAAGTAAATGGAATCAAAATTAATTTGCT 803  
Db 760 GCTAAATGCGCTGCTGCAAGCTGCAAGCTGCAAGCTGCAAGTAAATGGAATCAAAATTAATTTGCG 819  
Qy 804 GGATGAATTTCAAAATTTGTTGCAAGTTATTTATATCTGAGGCTATGTTTGTGCAAC 863  
Db 820 AGA-GTATTTTCAAAATTTGTTGCAAGTTGTTTATCTCAGGCTATG-TTGTGCAAC 877  
Qy 864 TTTATATATTTAAAGTCAAAATTAATGTTATGATATATAGTAAATAA 913  
Db 878 TTTATTTTAAAGTATTTTAAATTTAAATTTAAATTTAAATTTAAAGAA 927

RESULT 3  
US-09-765-213A-5  
; Sequence 5, Application US/09765213A

Patent No. US20020079846A1  
; GENERAL INFORMATION:  
; APPLICANT: Facchini, Peter J  
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides and Methods of Use  
; FILE REFERENCE: 22542-001  
; CURRENT APPLICATION NUMBER: US/09/765,213A  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/176708  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Papaver somniferum  
US-09-765-213A-5

Query Match 31.4%; Score 288; DB 9; Length 896;  
Best Local Similarity 59.6%; Pred. No. 1.8e-64;  
Matches 486; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

Qy 96 GGACTTCAGGGCTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGCTGCAGATTGGCCCT 155  
Db |||||  
Qy 81 GGAGTAAAGATTTAGTGTGATGCCCAAGTCCATTTGTGATGAGGCTAGAAITGGCACT 140  
Db |||||  
Qy 156 TAACCTCAAGGGTTTGGATTATGAGTGTGTTGAAGAGACTTTGAAATCCCAAAAGTGAAT 215  
Db |||||  
Qy 141 CAACATTAATCACTCAAGTATATCTTCTTGAAGAGACATTTGGTAGCAAAAGTGAAT 200  
Db |||||  
Qy 216 GCTTCTTAAGTCCAAACCTGTGCACAGAAATCCAGTTTCTTCCATGGAGATAAGT 275  
Db |||||  
Qy 201 TCTTCTGAAATCAATCCTATTTCAGAAATTTCTGTATGATTCATGGTGATNAACC 260  
Db |||||  
Qy 276 CATATGTAATCTGCAATCATGTTGATGATGATGAGTGTGTTGGTCCAAATGCTCT 335  
Db |||||  
Qy 261 CATCTGTAATCAATGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 320  
Db |||||  
Qy 336 CTCATCCTTCCCAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 395  
Db |||||  
Qy 321 TTCTATCATCCGCTGATCCTTATGATGCTTCCATGCTGCTGCTTCTGGGCAACCTACAT 380  
Db |||||  
Qy 396 CGATGACAGTGGCTTAGCTCTTGAAGAGTGTCTAGCGACTCAAGATGATGAGGCAAA 455  
Db |||||  
Qy 381 TGATGACAAAGTCTTTCGCTCTTAATGGGGAATTCGCAAGAGTAAAGATGAGAGAGAAA 440  
Db |||||  
Qy 456 GAAGCTACATTTGAGCAAGCGGAAGAGTCTTGGAGAGTGAAGAGTGTTCACAA 515  
Db |||||  
Qy 441 AAAAGCGCCATGAAACAGGCGATGACGCTTTGGTATCTGGAAGAGCTTATCAGAA 500  
Db |||||  
Qy 516 GTGAGTGAAGGAGGCTTATTTCCGAGGAGATACGATTTGGATTTGTTGACATTTGGTTT 575  
Db |||||  
Qy 501 AACTAGTAAAGAAAGACTTTTTCGGGGAAGAAAATTCGATACATTTGATATTGCATT 560  
Db |||||  
Qy 576 TGAAGCTTTTGGATTTTTCATGAGTCTCAGAGATTAAGTAAAGAAATTTGCTTGA 635  
Db |||||  
Qy 561 TGGGTGTTATATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620  
Db |||||  
Qy 636 TGAACAGAGTACCTGCTTTGACCCATGAGTGTGCAATTTTCTGCTGATCCTGCTGT 695  
Db |||||  
Qy 621 TGAACAAAGATTCAGGCTTTACAAAATGGGCTGAGAAAATTTGTGAGATGAGACAGT 680  
Db |||||  
Qy 696 GAAGGGCTTCTGCCAGAGACTGAAAAGCTTTGTTGAGTTTCCAAAGATTTCTCAGTAAA 755  
Db |||||  
Qy 681 TAATCTGTTATGCTGAACTGATGCTCTCATGGAGTTTCTGAGAGATCTTTGGATC 740  
Db |||||  
Qy 756 ATGGGCTGCTGAGTCTGCAAGTAAATGGAATCAAAATTAATGCTGGAGATTTTCA 815  
Db |||||  
Qy 741 TAAGCTCTCTCTTCAAACTAGAAAAGTGTGTAACAAATGAAATATCTTAGAGATGTTA 800  
Db |||||  
Qy 816 AAAATGTTGCAAGTATTTATATCTGAGGCTATGTTGTTGCAACTTTATATATTA 875  
Db |||||  
Qy 801 AGCTTTGTGTTGTTTTTTCAGTGTGTGTGATGATGCTTAAGAACTGTTTGTAGAAATG 860  
Db |||||

Qy 876 AAAGTCAAAATTAATGTTATGATAATATAGTAAAAA 911  
Db 861 ATCAGAACACAGTCTGCTGTAATAAAAAAAAAAAAA 896

## RESULT 4

US-09-765-213A-1  
; Sequence 1, Application US/09765213A  
; Patent No. US20020079846A1  
; GENERAL INFORMATION:  
; APPLICANT: Facchini, Peter J  
; TITLE OF INVENTION: No. US20020079846A1e1 Glutathione-S-Transferase Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides and Methods of Use  
; FILE REFERENCE: 22542-001  
; CURRENT APPLICATION NUMBER: US/09/765,213A  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/176708  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 998  
; TYPE: DNA  
; ORGANISM: Papaver somniferum  
US-09-765-213A-1

Query Match 29.4%; Score 270; DB 9; Length 998;  
Best Local Similarity 63.6%; Pred. No. 9.3e-60;  
Matches 411; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

Qy 97 GACTTGAGGCTTTGGGTGCTTGGTTCAGTCCATTTGCCCTGAGGCTGCAGATTGGCCCT 156  
Db |||||  
Qy 99 GAGGTGAAGATTTTAGTGTGATGCCCAAGTCCATTTGTGATGAGGCTTAGAAITGGCACT 158  
Db |||||  
Qy 157 AACCTCAAGGTTTGGGATTAAGTGTGTTGAAGAGACTTTGAAATCCCAAAAGTGAATTG 216  
Db |||||  
Qy 159 AACATTAATCAGTCAAGTATATCTTCTTGAAGAGACATTTGGTAGCAAAAGTGAAT 218  
Db |||||  
Qy 217 CTTCTTAAGTCCAAACCTGTGCACAGAAATCCAGTTTCTTCCATGGAGATAAGTGC 276  
Db |||||  
Qy 219 CTTCTGAAATCAAAATCCTATTTCACAGAGATGCTGCTTGTATTTCAGGCTGATAAACCC 278  
Db |||||  
Qy 277 ATATGTAATCTGCAATCATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 336  
Db |||||  
Qy 279 ATCTGTGAATCAATGATCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 338  
Db |||||  
Qy 337 TCCATCCTTCCACAAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396  
Db |||||  
Qy 339 TCCATCATCCTTCTGATCCTTATGATGCTTCCATGCTCGTTTCTGGCAACCTACATT 398  
Db |||||  
Qy 397 GATGACAAAGTGGCTTACGTCCTTGAAGAGTGTCTTAGCGACTGAAGATGATGAGGCAAG 456  
Db |||||  
Qy 399 GATGACAAAGTCTTTCCTGCTCTTTAATGGGATTCGAAAGAGTAAAGGATGCAAGAGAAA 458  
Db |||||  
Qy 457 AAGCTACACTTTGAGCAAGCGGAAGAGTGTCTGAGAGGTTGGAAGAGTGTTCACACAG 516  
Db |||||  
Qy 459 AAAGCAGCCATTGAACAGGCGATTCGAGCTTTTCGTATCTTGAAGAGCTTATCAGAAA 518  
Db |||||  
Qy 517 TGCAGTGAAGGAGGCTTATTCGAGGAGATACGATTTGGATTTGTTGACATTTGGTTT 576  
Db |||||  
Qy 519 ACTAGTAAAGAAAGATTTTTTTCGGTGAAGAAAATTTGGGTATGTCGATTTGCAATTT 578  
Db |||||  
Qy 577 GGAAGCTTTTGGATTTTTCATTAGAGTCTCAGAGATATGAATGAAGAAATTTGCTTGAT 636  
Db |||||  
Qy 579 GGGTGTATGTTGGCTGGAATTAGAGTTACAGAGAAAGTGAACGGAATCAAACTATTGAT 638  
Db |||||  
Qy 637 GAAACGAGTACCTGTTGACCCATGCGCTGAAACTTTTGTCTGATCCTGCTGTG 696  
Db |||||  
Qy 639 GAAGAAAAGTTCAGGGCTTTACAAAATGGGCTTACAAAATTTGTGCTGATGACAGATT 698  
Db |||||  
Qy 697 AAGGCTTCTGCGCAGAGACTGAAAAGCTTCTGATTTGCAAGA 742  
Db |||||

Db 699 AATCTGTTATGCTGAAACTGATGCCCTCATGGAGTTTGCTAAGA 744

RESULT 5

US-09-765-213A-3  
; Sequence 3, Application US/09765213A  
; Patent No. US20020079846A1  
; GENERAL INFORMATION:  
; APPLICANT: Facchini, Peter J  
; TITLE OF INVENTION: Polypeptides and Methods of Use  
; FILE REFERENCE: 22542-001  
; CURRENT APPLICATION NUMBER: US/09/765,213A  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/176708  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 947  
; TYPE: DNA  
; ORGANISM: Papaver somniferum  
US-09-765-213A-3

Query Match 29.2%; Score 268.4; DB 9; Length 947;  
Best Local Similarity 63.5%; Pred. No. 2.4e-59;  
Matches 410; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

Qy	97	GACITGAGGCTTTGGGTGCTTGGTTGAGTCCATTTGCCCTGAGGTCGACATTTGCCCTT	156
Db	48	GAGGTGAAGATTTTAGGTGGATGGCCAAAGTCCATTTGTGATGAGGCTTAGAATTTGCACTC	107
Qy	157	AACCTCAAGGTTTGGATTATGAGTGTCTGAAGAGACTTTTGAATCCCAAGTGAATTG	216
Db	108	AACATTAATCAGTCAAGTATATCTCTTGAGAGACATTTGGTAGCAAAAGTGAATTT	167
Qy	217	CTTCTTAAGTCCAAACCTGTGCACAAAGAAATCCAGTTTCTTCCATGGAGATAAAGTC	276
Db	168	CTTCTGAATCAATCTTATTTACAAAGAGATGCTGTCTTGAATTCACGGTGAATAAGCC	227
Qy	277	ATATGTGAATCTGCAATATAGTTGAGTACATAGATGAGGTTTGGTCCAAACATGCTCTC	336
Db	228	ATCTGTGAATCAATGATCATTTGTTTCAGTACATTTGATGATGTCTGGGCTTCTGCTGGTCA	287
Qy	337	TCCATCTCTTCCAAAAATGCATATGATCGAGCTAATGCGCATTTTGGGTTTCTTACATC	396
Db	288	TCCATCATCCCTTCTGATCCTTATGATGCTTCCATTTGCTCTGCTGGGCAACCTACATTT	347
Qy	397	GATGACAAAGTGGCTTTACGTCTTGAAAGTGTCTTAGCGACTGAAGATGATGAGGCAAG	456
Db	348	GATGACAAAGTCTTTCCGCTCTTTAATGGGGATTGCAAAGAGTAAAGGATGCAGAAAGAAA	407
Qy	457	AAGCTACACTTTGAGCAAGCGGAAGTGTCTGAGAAGGTGGAAGAGTGTTCACAAAG	516
Db	408	AAAGCAGCCATTGACAGCGGATTTGCAGCTTTTGGTATACCTTGAAGAAGCTTATCAGAAA	467
Qy	517	TGCAGTGAAGGGAAGGCTTATTTCCGAGGAGATACGATTTGATTTGTTGACATTTGTTTT	576
Db	468	ACTAGTAAGGAAGAAGATTTTTTTCGGTGGAGAAAATTTGGGTATGTCGATTTGCAATTT	527
Qy	577	GGAAAGCTTTTGGATTTTCATTTAGAGTCTCAGAGAAATATGAATGAAGAAAATTTGCTTGAT	636
Db	528	GGGTGTTATGTTGGCTGATTTAGAGTTACAGAGAAGATGAACCGAATCAAACTATTTCAT	587
Qy	637	GAAAGGAAGTACCTGGTTTGAACCTTATGGGCTGAAACTTTTGTGCTGATCCTGCTGTG	696
Db	588	GAAAGAAAAGTTTCCAGGGCTTTACAAAATGGGCTGAGAAAATTTTGTGCGAGATGAGACGGTT	647
Qy	697	AAGGGCTTCTGCGAGAGACTGAAAGCTTCTTGAGTTTGCAGAA 742	
Db	648	AAATCTGTTATGCTGAAACTGATGCCCTCATGGAGTTTGCTAAGA 693	

RESULT 6

US-10-021-323-17539  
; Sequence 17539, Application US/10021323  
; Publication No. US20040123340A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(52274)B  
; CURRENT APPLICATION NUMBER: US/10/021,323  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880  
; SEQ ID NO 17539  
; LENGTH: 671  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(671)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3831-001-Q1-K6-B3  
US-10-021-323-17539

Query Match 27.1%; Score 249.2; DB 17; Length 671;  
Best Local Similarity 65.2%; Pred. No. 2e-54;  
Matches 431; Conservative 0; Mismatches 219; Indels 11; Gaps 4;

Qy	124	AGTCATTTGCGCTGAGGGTGCGAGATTGCGCTTAACTCAAGGGTTTGGATTATGAGGTT	183
Db	5	AGTCATATGGATGAGGCCCAAGNATTTGCCCTTAACCTCAATCCCTCCTTACGAATAC	64
Qy	184	GTTGAAGAGACTTTT---GAATCCCAAAAGTGAATTGTTCTTAACTCAAGCTTCCAAACCTGTGCAC	240
Db	65	ATTGAAGAGAAATTATGGGAAGGCCAAAGCGAGCTTCTTCTCAATCAAAACCTGTGTAC	124
Qy	241	AAGAAATCCAGTTTTTCTTCCATGGAGAT---AAGTCATATGTGAATCTGCAATCATA	297
Db	125	AAGAAATCCAGTCTTCATTCACGGCGATAACAAAGCCAATCTGCGAATCTCTCATCATC	184
Qy	298	GTTGAGTACATAGATGAGGTTTGGTCCAAACATGCTCTCTCCATCTTCCACAAAATGCA	357
Db	185	GTACAATACATCGACGAGGCTTGGTCTTCC---GGTCTTCTATTCTTCTCTGATCCC	241
Qy	358	TATGATCGAGCTAATGCCGATTTTGGGTTTCTTACATCGATGACAAAGTGGCTTACGTCC	417
Db	242	TGTGAACGTGCTGCTCGCTCGGTTTGGGCTGCATATCTTGACGACAAAGTGGTCCAGCG	301
Qy	418	TTGAAAGTGTCTTAGCGACTGAAGATGATGAGGCAAGAGCTACACTTTGACGACGCG	477
Db	302	GTGAAAAGTATAGAGTTCGCTTAAAGGAGAGCAAGAAAGCAAGCAATAGCCCAAGTG	361
Qy	478	GAAGAGTGTCTGAGAAGGTGGAAGAGTGTTCACAAAGTGCAGTGAAGGGAAGGCTTAT	537
Db	362	GAAGCGGGTGGCTTTGATGGAGAAGCAATACGCAAGTGCAGCAAGGGAAGGGGTATC	421
Qy	538	TTGAGGAGATACGATTTGGATTGTTTGACATTTGGTGGTGGTGGTGGTGGTGGTGGTGGT	597
Db	422	TTTGGTGGGATGAAGTTGGTACCTTGTATATAGCTTTTGGAGCTTCTTGGGATGGCTT	481
Qy	598	AGAGTCTCAGAGATATGAATGAAAGAAATTTGCTTGTATGAAAGAGAGTACCTTGGTTTG	657
Db	482	AGAGTGAAGGAGAGTTCATTCGATGCGATGAAGTGTGTCGACGAGGGAAGACGCTTGGTCTG	541
Qy	658	ACCTATGGGCTGAAACTTTTGTGCTGATCCTGCTGCTGAGGGCTTCTTCCAGAGACT	717
Db	542	GTAATATGGGCGGACAGGTTCTGTTCCATGCGCTGTGAAGGATGTTATGCTGATACT	601
Qy	718	GAAAAGCTTGTGAGTTTGCAAGATTCT--TCAGCTTAAATGGGCTGCTGCAAGCTGCTG	775

Db 602 GACAGCTTGGGAGTTTGGTAAGTTTCTATTCCCAATAGGCGCTGGCGCTGCTG 661  
Qy 776 C 776  
Db 662 C 662

RESULT 7  
US-09-938-842A-2676  
; Sequence 2676, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2676  
; LENGTH: 684  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2676

Query Match 26.1%; Score 240; DB 9; Length 684;  
Best Local Similarity 59.6%; Pred. No. 5e-52;  
Matches 405; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

Qy 85 ATGGCTGAAAGGACTTTGAGGCTTTTGGGTGCTTTGGTTTCAGTCCATTTGCCCTGAGGGTG 144  
Db 1 ATGGCGACCGGAGGAGCTGAGCTGATCGGCTCATGGCGAGTGTTTACGTTCATGAGGCG 60

Qy 145 CAGATTGCCCTTAACCTCAAGGGTTTGGATTATGAGTTTGAAGAGACTTTGAATCCC 204  
Db 61 AGGATCGCTCTCCACCTCAAACTATTAGCTACGAATTCCTTCAGGAGAGCTATGGTTCA 120

Qy 205 AAAAGTGAATTTGCTTTTAACTCAACCTGTGACAAAGAAATCCCAAGTTTCTCCAT 264  
Db 121 AAGAGCGAATTTGCTTCAAAATCAAAACCCGGTTCAAGAAGATGCCGGTTCTGATTCA 180

Qy 265 GGAGATAAAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGTTTGGTCC 324  
Db 181 GCTGACAAACCGGTGTCGAGTCCAACTCATCTTATATCGAGAGGCTTGGAAAC 240

Qy 325 AACAAATGCTCTCTCCATCTTCCAAATAATGCATATGATCGAGTAAATGCCGAGTTTGG 384  
Db 241 TCTTCTGGACCTTCCATCTTCCCGTCCCATCCATACGACCGGGCCATTGCTCGGTTTGG 300

Qy 385 GTTCTTACATCGATGACAGTGGCTTACGCTTGAAGAGTGTCTAGCGACTGAAGAT 444  
Db 301 GCTGCCCTACATAGACGATCAGTGGTTTATCTCTGTGAGAAGTATCCCTAACAGCTCAAGGA 360

Qy 445 GATGAGCAAGAAGAGCTACACTTTGAGCAACCGGAAGAGTGTCTGAGAAGTTGGAAGAA 504  
Db 361 GACGAGAGAAGAAGAGCTCAAGTGTGAGAAGAGCAAGCTTCTGGAGAA 420

Qy 505 GTGTTCAACAGTGCAGTGAAGGAGGCGCTTATTTCCGAGAGATACGATTGAGTTTGT 564  
Db 421 GCATTCAACGATTGTAGCCAGGAAACCGTTCTTCAACCGGTGACCATATCGGTTACCTC 480

Qy 565 GACATTGGTTTGAAGCTTTTTCAGTTTCATTAGACTCTCAGAGATATGAATGAAGA 624

Db 481 GACATTGCCCTTGGGAGCTTCTTAGGTTGTGGAGAGTCTGCGAGTTGGATGCCAATCAT 540  
Qy 625 AAATTGCTTGATGAACGAAGTACCTGTTGTTGACCTATGCGCTGAACATTTTGTCTGCT 684  
Db 541 AAATTTCTTGATGAGACCAAACTCCCTCTCTAGTCAAAATGGGAGAGCGGTTCTGTGAT 600  
Qy 685 GATCCTGCTGTGAAGGCGCTTCTGCCAGAGACTGAAAGCTTGTGTGAGTTTGCAAGATT 744  
Db 601 GATCCCGCTGTGAACCTATATATGCGCGAGATTACAAGCTCGCTGATTCGCAAGGAG 660

Qy 745 CTTGAGCTAAAAATGGGCTGC 764  
Db 661 CTCTTTCTTAAGCGCAAGC 680

RESULT 8  
US-09-938-842A-2676  
; Sequence 2676, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2676  
; LENGTH: 684  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2676

Query Match 26.1%; Score 240; DB 11; Length 684;  
Best Local Similarity 59.6%; Pred. No. 5e-52;  
Matches 405; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

Qy 85 ATGGCTGAAAGGACTTTGAGGCTTTTGGGTGCTTTGGTTTCAGTCCATTTGCCCTGAGGGTG 144  
Db 1 ATGGCGACCGGAGGAGCTGAGCTGATCGGCTCATGGCGAGTGTTTACGTTCATGAGGCG 60

Qy 145 CAGATTGCCCTTAACCTCAAGGGTTTGGATTATGAGTTTGAAGAGACTTTGAATCCC 204  
Db 61 AGGATCGCTCTCCACCTCAAACTATTAGCTACGAATTCCTTCAGGAGAGCTATGGTTCA 120

Qy 205 AAAAGTGAATTTGCTTTTAACTCAACCTGTGACAAAGAAATCCCAAGTTTCTCCAT 264  
Db 121 AAGAGCGAATTTGCTTCAAAATCAAAACCCGGTTCAAGAAGATGCCGGTTCTGATTCA 180

Qy 265 GGAGATAAAGTCATATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGTTTGGTCC 324  
Db 181 GCTGACAAACCGGTGTCGAGTCCAACTCATCTTATATCGAGAGGCTTGGAAAC 240

Qy 325 AACAAATGCTCTCTCCATCTTCCAAATAATGCATATGATCGAGTAAATGCCGAGTTTGG 384  
Db 241 TCTTCTGGACCTTCCATCTTCCCGTCCCATCCATACGACCGGGCCATTGCTCGGTTTGG 300

Qy 385 GTTCTTACATCGATGACAGTGGCTTACGCTTGAAGAGTGTCTAGCGACTGAAGAT 444  
Db 301 GCTGCCCTACATAGACGATCAGTGGTTTATCTCTGTGAGAAGTATCCCTAACAGCTCAAGGA 360

Qy 445 GATGAGCAAGAAGAGCTACACTTTGAGCAACCGGAAGAGTGTCTGAGAAGTTGGAAGAA 504  
Db 361 GACGAGAGAAGAAGAGCTCAAGTGTGAGAAGAGCAAGCTTCTGGAGAA 420



```
Db 191 ACAAACGATGTCGAGTCTCTCAACATCGTTGAATACATGATGAGACGTGGACTCAT 250
Qy 329 ATGCTCTCTCCATCTTCCACAAATGCATATGATGAGCTTAATGCCCGATTTTGGGTTT 388
Db 251 CTGCACCGTCATCTCTCTCCATCATCTTATGATCGTCTCTGCTCGCTTTTGGTCTG 310
Qy 389 CTTACATCATGATGACAGTGGCTTACGTCCTTGAAGAGTGTCTTAGCGACTGAGATGATG 448
Db 311 ACTTCGTTGATTAACAAGTGGTTTCCGGCGTTTGAGAAATGGCGCGATCACTAAATCGGAAG 370
Qy 449 AGGCAAGAGAGTACACTTTTGAGCAAGCGGAAGAGTGTGAGAAAGTGGGAAGAGTGT 508
Db 371 AGCAGAAAGCGAAGCCATGGAAGAGTGGGAAGAGTGTGTCGAATCGAGATCGGT 430
Qy 509 TCAACAAGTGCAGTGAAGGAGGAGCCCTATTTCGGAGGAGATACGATTTGGAATTTTGACA 568
Db 431 TTGTTTCTATAAGCAAGGAGGAAACCCCTTTTCGGCGGTGAGCAATCGGTTTATGATA 490
Qy 569 TTGTTTTGGAGCTTTTGTAGTTTCAATGATGCTCAGAGAAATATGAATGAAGAAAT 628
Db 491 TTTGCTTTGGAAGCTTTGTGTTCTCTTGAAGCTAGAGAAAGTTTAAAGCAGAAAGC 550
Qy 629 TGCTTGATGAACCAAGTACCTGTTTGAACCTATGACCTATGCGCTGAACTTTTGTCTGCTGATC 688
Db 551 TTTTAGACGAATCAAAACTCTCTCTTTGTAAGTGGCGCGAGATCGAAGAGTGTGCTTCTACAGAACTTG 670
Qy 689 CTGCTGTAAGGGGCTTCTGCGAGAGACTGAAAGCTTTGAGTGTGTTGAGTTTGCAGAAATTTCTC 748
Db 611 AAACGGTGAAGATGTGGCACCGAGATCGAAGAAAGTGTGAGTGTGCTTCTACAGAACTTG 670
Qy 749 AGCTAAATGGGCTGTGCTGAGCTGC 773
Db 671 AGGTTAGAGCTCAATCGCAGCTTC 695
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## RESULT 11

```
US-09-770-445-743/c
; Sequence 743, Application US/09770445
; Patent No. US2002023281A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Gorch, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
```

## TITLE OF INVENTION: Expressed Sequences of Arabidopsis

```
; Publication No. US20040016025A1
```

## FILE REFERENCE: 2023US (PARA-012PRV)

```
; CURRENT APPLICATION NUMBER: US/09/770,445
```

```
; CURRENT FILING DATE: 2001-01-26
```

```
; PRIOR APPLICATION NUMBER: US 60/178,472
```

```
; PRIOR FILING DATE: 2000-01-27
```

```
; NUMBER OF SEQ ID NOS: 999
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 743
```

```
; LENGTH: 817
```

```
; TYPE: DNA
```

```
; ORGANISM: Arabidopsis thaliana
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(817)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-743
```

Query Match 24.9%; Score 228.2; DB 9; Length 817;

Best Local Similarity 59.3%; Pred. No. 6.6e-49;

Matches 396; Conservative 0; Mismatches 269; Indels 3; Gaps 1;

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Qy 70 TTATAGTAAACAGTGTGCTGAAAGGAGCTTGAGGCTTTTGGGTGCTTGGTTCAGTCCA 129
Db 817 TTAGACAAAACAAAGATGGTAGAGAGAGAGGTGAAACTGTGTGGAAACATGATACAGTCCG 758
Qy 130 TTTGCCCTGAGGGTGCAGATGTCCTTAACCTCAAGGGTTTGGATTTATGAGTTGTTGAA 189
Db 757 GTCGTGATAAGAGTAAAGATCGCTCTCAAAATCGGTTGATTTATGATTACGTTGAA 698
Qy 190 GAGACTTTTG--AATCCCAAAAGTGAATTCCTTAAAGTCCAAACCTGTGCACAAGAAA 246
Db 697 GAGAACTTGTTCGATCTAAGAGTGAAGTCTTCTCAATCGAACCCGGTTTACAGAAA 638
Qy 247 ATCCAGTTTTCTTCCATGGAGATAAAAGTCAATATGTGAATCTGCAATCATAGTTGAGTAC 306
Db 637 GTCCCGTTCTCATCCACAGTAAATCGGTTGTGAGTCTCTAAACATCGTTGAATAC 578
Qy 307 ATAGATGAGTGTGCTCCAAACATGCTCTCCATCCTTCCACAAAATGCATATGATCGA 366
Db 577 ATAGACGAGAGCTGGAACTCATCTGGATCGTTCAATCTCTTCTCATCTCATGATCGT 518
Qy 367 GCTAATGCCCGATTTTGGGTTTCTTACATCGATGACAAGTGGCTTAGCTCTCGAAAAGT 426
Db 517 GCCCTTGTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458
Qy 427 GTTCTAGCGACTGAAGATGATGAGGCAAGAAAGTACACTTTTGAGCAAGCGGAAAGAGTG 486
Db 457 GCTGTGCTGCTAAATCGGAAGACGCAAAAGCAAAAGGATGGAAGAAAGTGAAGAAAGG 398
Qy 487 CTTGAGAAAGTGGAAAGTGTTCACAAAGTGCATGCTGAGGAGGAGGCTATTTTCGGAGGA 546
Db 397 TTGTTGCAACTCGAAGCTGCGTTTATTGCTCTAAGCAAGGAAAGAAATCTTTTTCGGCGGT 338
Qy 547 GATACGATTCGATTTGTTGACATTTGTTGGAAGCTTTTGTAGTTTTCATTAGAGTCTCA 606
Db 337 GAAACAATCGGTTTCATAGACATTTGCTTGGAAAGCTTTTGTGTTTCTTGAAGCTAGA 278
Qy 607 GAGAAATATGAATGAAGAAAGAAATTCCTTGTATGAAACGAAAGTACCTTGTGTTGACCTATGG 666
Db 277 GAGAGCTTAAAGAAAGNNNNNATTTAGACGAAATNNAAAACTCTCTCTTTATAGATGG 218
Qy 667 GCTGAAACTTTTGTGCTGCTGATCTGCTGCTGAGGCGCTTCTGCCAGAGACTGAAAAGCTT 726
Db 217 GCCAACCGNNNTTTGTCAGATGAAACAGTGAAGAAATGTGGTGGCGGAGATAGATAAAGTT 158
Qy 727 GTTGAGTT 734
Db 157 GCCAAGCT 150
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## RESULT 12

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US-10-260-238-4937/c
; Sequence 4937, Application US/10260238
```

```
; Publication No. US20040016025A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Budworth, Paul R.
```

```
; APPLICANT: Moughamer, Todd G.
```

```
; APPLICANT: Briggs, Steven P.
```

```
; APPLICANT: Cooper, Bret
```

```
; APPLICANT: Glazebrook, Jane
```

```
; APPLICANT: Goff, Stephen A.
```

```
; APPLICANT: Katagiri, Fumiyaki
```

```
; APPLICANT: Kreps, Joel
```

```
; APPLICANT: Provart, Nicholas
```

```

; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 4937
; LENGTH: 779
; TYPE: DNA
; ORGANISM: Musa acuminata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (615)..(615)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (627)..(627)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (642)..(642)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (644)..(644)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (670)..(670)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (711)..(711)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (718)..(718)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (738)..(738)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (743)..(743)
; OTHER INFORMATION: n = any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (772)..(772)
; OTHER INFORMATION: n = any nucleotide
; US-10-260-238-4937
;
; Query Match 24.3%; Score 222.8; DB 16; Length 779;
; Best Local Similarity 56.9%; Pred. No. 1.6e-47;
; Matches 389; Conservative 0; Mismatches 295; Indels 0; Gaps 0;

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```

Qy 87 GGCTGAAGGACTTGAGGCTTTTGGTGTCTTGGTTCAGTCCATTGCCCTGAGGGTCA 146
Db 735 GCGGCGAGGAGAGTGTGANGCTGATNGGGGCGTGGCCGAGCCCGTCTGCTGCCCGCAG 676
Qy 147 GATTGCCCTTAACCTCAAGGGTTTGATTTATGAGTTTGTGAAGAGACTTTGAATCCAA 206
Db 675 GGTGNCCTCAACCTGAAGGGGTGGAGTACNANTTCTGCAGGAGAAATTCGGGGAGAA 616
Qy 207 AAGTGAATTGCTTTTAAAGTCCAAACCTGTGCAAGAAATCCAGTTTTCCTCCATGG 266
Db 615 NAGCGAGCTNCTTCTCAGATCCAAACCTGTGTACAAGAAGATCCCGTCTCTCCACCA 556
Qy 267 AGATAAGTCAATGTGAATCTGCAATCATAGTTGAGTACATAGATGAGTTTGGTCCA 326
Db 555 CGAAGAGCCCTTCGCGAGTGCATCGTGGAGTACGTGCGAGGCTCTGCGGCTTNGGCTAA 496
Qy 327 CAATGCTCTCTCCATCCCTCCACAAATGCAATGATCGAGCTAATCCCGATTTTGGGT 386
Db 495 TTCGGCCAGGNCATCTTNCCTGCCGACCCCTACGAGCGGCGNCCCTCCACCGCTTCTGTC 436
Qy 387 TTCTTACATCGATGACAAGTGGCTTACGTCTTGAAAAGTGTCTTAGCGACTGAAGATGA 446
Db 435 CGTCTACATCGACGACAAGTGGTTCCTCGTCAATATTCNGCATCGAAAAGGCTGAAACAGA 376
Qy 447 TGAGGCAAGAAGCTACATTTTGAGCAAGCGGAAGAGTCTTTGAGAGGTGGAGAGT 506
Db 375 GGAGGCCAAGGCCGAATCCCGAGCAAGCGTGGGCGGCTGAAGTGTCTCGAGGAGGC 316

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Db 367 CCAGTCCCGATTGCGGCGCTATGTCGAAGATAAGTTTCCACTGCTTAAGAAGAGT 426
Qy 429 TCTAGCAGCTGAAGATGATAGGCAAGCAAGCTACACTTTCAGCAAGCGGAAGTGCT 488
Db 427 GTTGTGCTGCTACAGAGGAGATATAAAGGCGCAGCAATGCCGAAGTCTCAGAAAGGAT 486
Qy 489 TGAGAAGGTGGAAGAAGTGTTCACCAAGTGCAGTGAAGGAGGCTATTTCCGAGGAGA 548
Db 487 GGTGCTGTTGGAGGAAGTCTTGTGCAATTCAGCAAGGGAAGCTTCTTTGGTGGGA 546
Qy 549 TACGATTCGATTTGTGACATGTTTGGAAAGCTTTTGTAGTTTCATAGAGT 602
Db 547 AAATATTGGTTTCGTGGACATAGTGTTCGGTAGCTTGTTCGGTGGATGAAGT 600
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## RESULT 15

```
US-10-021-323-15323
; Sequence 15323, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Peng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 15323
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-024-Q6-K6-G7
US-10-021-323-15323
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Query Match 22.5%; Score 206.6; DB 17; Length 589;
Best Local Similarity 65.0%; Pred. No. 2.4e-43;
Matches 370; Conservative 0; Mismatches 189; Indels 10; Gaps 4;
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```
Qy 107 TTTTGGGTGCTGTTTCAGTCCATTGTCCTGAGGTCAGATTGCCCTTAACCTCAAG 166
Db 24 TTTTGGGTTCCTGGCCGAGTCCATATGCGATGAGGCCAAGGATTGCCCTTAACCTCAAT 83
Qy 167 GTTTGGATTATGAGTTCTTGAAGAGACTTT---GAATCCCAAAAGTGAATTGCTTCTTA 223
Db 84 CCCTCACTTACGATATACATTGAGAGAGATTATGGGAAGGCAAAAGCGAGCTTCTCTCC 143
Qy 224 AGTCAACCTGTGCACAAG-AAAATCCAGTTTCTTCCATGGAGAT---AAAGTCATA 279
Db 144 AATCAAAACCTGTTTACAAGTAAATCCAGTCTCTCATTACCGGGATAACAAGCCAATC 203
Qy 280 TGTGAATCTGAATCATAGTTGAGTACATAGATGAGTTTGGTCCCAATGCTCTCTCC 339
Db 204 TCGGAATCTCTCATCATCGTACAATACATCGACGAGGCTTGGTCTCTCC---GGTCCTTCT 260
Qy 340 ATCTCTTCCACAAAATGCAATATGATCGAGCTAATGCCGATTTTGGGTTTCTTACATGAT 399
Db 261 ATTCTTCTCTGATCCCTGTGAAGTGCTGTGCTGGTTTGGGCTGCATATCTTGAC 320
Qy 400 GACAAGTGGCTTACGTCCTTGAAAAGTGTCTAGCGACTGAAGATGATGAGGCAAGAAG 459
Db 321 GACAAGTGGTCCCAAGCGGTGAAAAGTATAGGAGTCGCTAAAGGAGAGAGCAAGAAA 380
Qy 460 CTACACTTTGACGACGAGAGAGTCTTGAAGAGGTGGAAGAGTGTTCACCAAGTGC 519
Db 381 GCAGCAATAGCCCAAGTGGAAAGGGGTTGGCTTTGATGGGAAGAAGCATACGCAAGTGC 440
```

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Qy 520 AGTGAAGGGAAGGCCTATTTCCGAGGAGATACGATTCGATTTGTTGACATTTGTTTGA 579
Db 441 AGCAAAAGGGAAGGTTACTTTGGTGGGATGAAGTTGGGTACCTTGTATATAGCTTTTGGG 500
Qy 580 AGCTTTTGTAGTTTCATTAGAGTCTCAGAGAAATATGAATGAAGAATAATTCCTTGA 639
Db 501 AGCTTCTTGGGATGGCTTGTAGTGACCGGAAGTTCAATCGATGAAGCTGCTCGACGAG 560
Qy 640 ACGAAGTACCTTGGTTTGGACCCCTATGGGC 668
Db 561 GGGNAGACGCTGCTGCTGTAATAATGGGC 589
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Job time : 536 secs